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Transmitted herewith for filing is a **Continuation-in-Part** of International Application No. PCT/US99/07333 which claims the benefit of U.S. Application No. 60/080,671, Filed April 3, 1998.

Inventor(s): Thomas Stormann, Lance G. Hammerland, Laura L. Storjohann, James G. Busby, James E. Garrett, Rachel T. Simin

Title: G-PROTEIN FUSION RECEPTORS AND CHIMERIC GABA_B RECEPTORS

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- 7 Page(s) Claims
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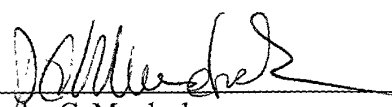
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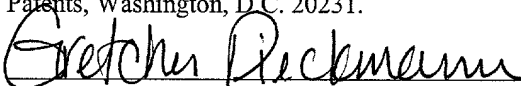
TITLE: G-PROTEIN FUSION RECEPTORS AND
CHIMERIC GABA_B RECEPTORS

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Gretchen Dieckmann

G-PROTEIN FUSION RECEPTORS AND CHIMERIC GABA_B RECEPTORS

RELATED APPLICATIONS

5 The present application is a continuation in part of PCT/US99/07333 which claims priority to Garrett *et al.* U.S. Serial No. 60/080,671, filed April 3, 1998, which is hereby incorporated by reference herein in its entirety including the drawings.

FIELD OF THE INVENTION

10 The present invention relates to a G-protein fusion receptors, chimeric GABA_B (γ -aminobutyric acid) receptors, nucleic acid encoding such receptors, and uses of such receptors and nucleic acid encoding such receptors.

BACKGROUND

15 The references cited herein are not admitted to be prior art to the claimed invention.

 Chimeric receptors made up of peptide segments from different receptors have different uses such as being used to assess the functions of different sequence regions and to assess the activity of different compounds at a particular receptor. Examples of using
20 chimeric receptors to assess the activity of different compounds are provided by Dull *et al.*, U.S. Patent No. 4,859,609, Dull *et al.*, U.S. Patent No. 5,030,576, and Fuller *et al.*, U.S. Patent No. 5,981,195.

 Dull *et al.* U.S. Patent No. 4,859,609, and Dull *et al.* U.S. Patent No. 5,030,576, indicate the production and use of chimeric receptors comprising a ligand binding domain
25 of a predetermined receptor and a heterologous reporter polypeptide. The Dull *et al.* patents provide as examples of chimerics: (1) a chimeric receptor made up of the insulin receptor extracellular chain, and the EGF receptor transmembrane and cytoplasmic domains without any HIR B-chain sequence; and (2) a hybrid receptor made up of the v-
erB oncogene product intracellular domain fused to the EGF receptor extracellular and
30 transmembrane domains.

 Fuller *et al.* International Publication No. WO 97/05252 feature chimeric receptors made up of metabotropic glutamate receptor (mGluR) domains and calcium receptor

(CaR) domains. The chimeric receptors allow the coupling of functional aspects of a mGluR with a CaR.

An example of the use of chimeric receptors to assess the functions of different sequence regions receptors are found in studies identifying regions of different guanine nucleotide-binding protein coupled receptors important for guanine nucleotide-binding protein coupling. (See, Kobilka *et al.*, *Science* 240:1310-1316, 1988; Wess *et al.*, *FEBS Lett.* 258:133-136, 1989; Cotecchia *et al.*, *Proc. Natl. Acad. Sci. USA* 87:2896-2900, 1990; Lechleiter *et al.*, *EMBO J.* 9:4381-4390, 1990; Wess *et al.*, *Mol. Pharmacol.* 38:517-523, 1990; and Pin *et al.*, *EMBO J.* 13:342-348, 1994.)

SUMMARY OF THE INVENTION

The present invention features G-protein fusion receptors and chimeric GABA_B receptors (GABA_BRs), nucleic acid encoding such receptors, and the use of such receptors and nucleic acid. G-protein fusion receptors comprise at least one domain from a CaR, a mGluR, and/or a GABA_B receptor fused directly or through a linker to a guanine nucleotide-binding protein (G-protein). Chimeric GABA_BRs comprise at least one of a GABA_BR extracellular domain, a GABA_BR transmembrane domain, or a GABA_BR intracellular domain and one or more domains from a mGluR subtype 8 (mGluR8) and/or a CaR.

G-proteins are peripheral membrane proteins made up of an α subunit, a β subunit, and a γ subunit. G-proteins interconvert between a GDP bound and a GTP bound form. Different types of G-proteins can affect different enzymes, such as adenylate cyclase and phospholipase-C.

Thus, a first aspect of the present invention describes a G-protein fusion receptor comprising:

an extracellular domain comprising an amino acid sequence substantially similar to either an extracellular CaR amino acid sequence, an extracellular mGluR amino acid sequence, or an extracellular GABA_B receptor amino acid sequence;

a transmembrane domain joined to the carboxy terminus of said extracellular domain, said transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to either a transmembrane CaR amino acid sequence, a transmembrane mGluR amino acid sequence, or a transmembrane GABA_B receptor amino acid sequence;

an intracellular domain joined to the carboxy terminus of said transmembrane domain comprising all or a portion of an intracellular amino acid sequence substantially similar to either an intracellular CaR amino acid sequence, an intracellular mGluR amino acid sequence, or an intracellular GABA_B receptor amino acid sequence, provided that
5 said portion is at least about 10 amino acids;

an optionally present linker joined to the carboxy terminus of said intracellular domain, where said optionally present linker is a polypeptide 3 to 30 amino acids in length, wherein said amino acids of the optionally present linker are selected from the group consisting of alanine, proline, serine, and glycine; and

10 a G-protein joined either to said intracellular domain or to said optionally present linker, provided that said G-protein is joined to said optionally present linker when said optionally present linker is present.

“Substantially similar” refers to at least 40% sequence similarity between respective polypeptide regions making up a domain. In preferred embodiments,
15 substantially similar refers to at least 50%, at least 75%, at least 90%, at least 95% sequence similarity, or 100% (the same sequence), between polypeptide domains. The degree to which two polypeptide domains are substantially similar is determined by comparing the amino acid sequences located in corresponding domains. Sequence similarity is preferably determined using BLASTN (Altschul *et al.*, *J. Mol. Biol.* 215:403-
20 410, 1990).

The different receptor components of the G-protein receptor can come from the same receptor protein or from a chimeric receptor made up of different receptor domains. By swapping different domains compounds able to effect different domains of a particular receptor can be identified and the activity of different compounds at different
25 domains can be measured.

In different embodiments the CaR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian CaR, preferably the human CaR; mGluR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian mGluR,
30 preferably a human mGluR; and GABA_BR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian GABA_BR, preferably a human GABA_BR.

In preferred embodiments concerning GABA_BR regions that are present: the GABA_BR extracellular domain is substantially similar to a GABA_BR extracellular domain provided in SEQ. ID. NOs. 2-4; the GABA_BR transmembrane domain is substantially similar to the GABA_BR transmembrane domain provided in SEQ. ID. NOs. 7-9; and the GABA_BR intracellular domain is substantially similar to a GABA_BR intracellular domain provided in SEQ. ID. NOs. 12-14.

In preferred embodiments concerning CaR regions that are present: the CaR extracellular domain is substantially similar to the CaR extracellular provided in SEQ. ID. NO. 1; the CaR transmembrane domain is substantially similar to the CaR transmembrane domain provided in SEQ. ID. NO. 6; and the CaR intracellular domain is substantially similar to the CaR intracellular domain such as that provided in SEQ. ID. NO. 11.

Various different mGluR subtypes present in different organisms, including humans, are described in different patent publications as follows: mGluR₁ - WO 94/29449, EP 569 240 A1, WO 92/10583 and U.S. Patent No. 5,385,831; mGluR₂ - WO 94/29449, WO 96/06167, and EP 711 832 A2; mGluR₃ - WO 94/29449, and WO 95/22609; mGluR₄ - WO 95/08627, WO 95/22609, and WO 96/29404; mGluR₅ - WO 94/29449; mGluR₆ - WO 95/08627; mGluR₇ - U.S. Patent No. 5,831,047, WO 95/08627 and WO 96/29404; and mGluR₈ - U.S. Patent Nos. 6,051,688, 6,077,675, 6,084,084 and EP 816 498 A2. (Each of these references are hereby incorporated by reference herein.)

In preferred embodiments concerning mGluR regions that are present: the mGluR extracellular domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8; the mGluR transmembrane domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8; and the mGluR intracellular domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8. Preferred embodiments also include any mGluR splice variant.

In preferred embodiments concerning the optionally present linker, said optionally present linker is a polypeptide 3 to 30 amino acids in length, wherein said amino acids of the optionally present linker are selected from the group consisting of alanine, proline, serine, and glycine; and more preferably, the optionally present linker is comprised of alanine amino acids.

Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a G-protein fusion receptor, and a cell where the G-protein fusion receptor is expressed. Preferably, the G-protein fusion receptor is functional in the cell.

5 Another aspect of the present invention describes a recombinant cell produced by combining (a) a cell where a G-protein fusion receptor is expressed, and (b) a vector comprising nucleic acid encoding a G-protein fusion receptor and elements for introducing heterologous nucleic acid into the cell. Preferably, the G-protein fusion receptor is functional in the cell.

10 Another aspect of the present invention describes a process for the production of a G-protein fusion receptor. The process is performed by growing host cells comprising a G-protein fusion receptor.

Another aspect of the present invention describes a method of measuring the ability of a compound to affect G-protein fusion receptor activity.

15 Another aspect of the present invention describes a chimeric GABA_BR comprising an extracellular domain, a transmembrane domain and an intracellular domain, wherein at least one domain is from a GABA_BR and at least one domain is from CaR or mGluR8. The extracellular domain comprises an amino acid sequence substantially similar to a CaR extracellular domain (SEQ. ID. NO. 1), a GABA_BR1a extracellular domain (SEQ. ID. NO. 2), a GABA_BR1b extracellular domain (SEQ. ID. NO. 3), a GABA_BR2
20 extracellular domain (SEQ. ID. NO. 4), or a mGluR8 extracellular domain (SEQ. ID. NO. 5).

The transmembrane domain comprises an amino acid sequence substantially similar to a CaR transmembrane domain (SEQ. ID. NO. 6), a GABA_BR1a transmembrane
25 domain (SEQ. ID. NO. 7), a GABA_BR1b transmembrane domain (SEQ. ID. NO. 8), a GABA_BR2 transmembrane domain (SEQ. ID. NO. 9), or a mGluR8 transmembrane domain (SEQ. ID. NO. 10).

The intracellular domain comprises an amino acid sequence substantially similar to a CaR intracellular domain (SEQ. ID. NO. 11), a GABA_BR1a intracellular domain
30 (SEQ. ID. NO. 12), a GABA_BR1b intracellular domain (SEQ. ID. NO. 13), a GABA_BR2 intracellular domain (SEQ. ID. NO. 14), or a mGluR8 intracellular domain (SEQ. ID. NO. 15).

Preferred chimeric GABA_BRs contain at least one mGluR8 intracellular, transmembrane or extracellular domain, or at least one CaR intracellular, transmembrane or extracellular domain. More preferably, the chimeric GABA_BR contains at least one CaR domain.

5 In preferred embodiments concerning mGluR8 regions that are present: the mGluR8 extracellular domain is substantially similar to the mGluR8 extracellular domain provided in SEQ. ID. NO. 5; the mGluR8 transmembrane domain is substantially similar to the mGluR8 transmembrane domain provided in SEQ. ID. NO. 10; and the mGluR8 intracellular domain is substantially similar to the mGluR8 receptor intracellular provided
10 in SEQ. ID. NO. 15.

Preferably, the domains are functionally coupled such that a signal from the binding of an extracellular ligand is transduced to the intracellular domain when the chimeric receptor is present in a suitable host cell. A suitable host cell contains the elements for functional signal transduction for receptors coupled to a G-protein.

15 Another aspect of the present invention describes a nucleic acid comprising a nucleotide sequence encoding for a chimeric GABA_BR.

Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a chimeric GABA_BR, and a cell where the chimeric GABA_BR is expressed. Preferably, the chimeric GABA_BR is functional in the cell.

20 Another aspect of the present invention describes a recombinant cell produced by combining (a) a cell where a chimeric GABA_BR is expressed, and (b) a vector comprising nucleic acid encoding the chimeric GABA_BR and elements for introducing heterologous nucleic acid into the cell. Preferably, the chimeric GABA_BR is functional in the cell.

Another aspect of the present invention describes a process for the production of a
25 chimeric receptor. The process is performed by growing host cells comprising a chimeric GABA_BR.

Another aspect of the present invention describes a method of measuring the ability of a compound to affect GABA_BR or mGluR activity. The method is performed by measuring the ability of a compound to affect chimeric GABA_BR or mGluR activity.

30 Another aspect of the present invention describes a fusion receptor polypeptide comprising a receptor and a G-protein α subunit, wherein said G-protein α subunit is fused to the intracellular domain of said receptor, provided that the receptor is not an adrenoreceptor.

Various examples are described herein. These examples are not intended in any way to limit the claimed invention.

Other features and advantages of the invention will be apparent from the following drawings, the description of the invention, the examples, and the claims.

5

BRIEF DESCRIPTION OF DRAWINGS

Figures 1a-1d illustrate the amino acid sequences of a human CaR extracellular domain (SEQ. ID. NO. 1), a human GABA_BR1a extracellular domain (SEQ. ID. NO. 2), a human GABA_BR1b extracellular domain (SEQ. ID. NO. 3), a human GABA_BR2
10 extracellular domain (SEQ. ID. NO. 4), and a human mGluR8 extracellular domain (SEQ. ID. NO. 5).

Figures 2a-2b illustrate the amino acid sequences of a human CaR transmembrane domain (SEQ. ID. NO. 6), a human GABA_BR1a transmembrane domain (SEQ. ID. NO. 7), a human GABA_BR1b transmembrane domain (SEQ. ID. NO. 8), a human GABA_BR2
15 transmembrane domain (SEQ. ID. NO. 9), and a human mGluR8 transmembrane domain (SEQ. ID. NO. 10).

Figures 3a-3b illustrate the amino acid sequences of a human CaR intracellular domain (SEQ. ID. NO. 11), a human GABA_BR1a intracellular domain (SEQ. ID. NO. 12), a human GABA_BR1b intracellular domain (SEQ. ID. NO. 13), a human GABA_BR2
20 intracellular domain (SEQ. ID. NO. 14), and a human mGluR8 intracellular domain (SEQ. ID. NO. 15).

Figures 4a-4b illustrate the amino acid sequence of G₁₅ (SEQ. ID. NO. 16) and G₁₆ (SEQ. ID. NO. 17).

Figures 5a-5r illustrate the cDNA sequences encoding for human CaR (SEQ. ID. NO. 18), human GABA_BR1a (SEQ. ID. NO. 19), human GABA_BR1b (SEQ. ID. NO. 20),
25 and human GABA_BR2 (SEQ. ID. NO. 21).

Figures 6a-6h illustrate the cDNA sequence for rat GABA_BR1a (SEQ. ID. NO. 22) and rat GABA_BR1b (SEQ. ID. NO. 23).

Figures 7a-7c illustrate the amino sequence for rat GABA_BR1a (SEQ. ID. NO. 24) and rat GABA_BR1b (SEQ. ID. NO. 25).
30

Figure 8 illustrates the ability of a chimeric CaR/GABA_BR2 (CaR extracellular and transmembrane domains, and intracellular GABA_BR2 domain) to transduce a signal. Signal production was measured by detecting an increase in the calcium-activated

chloride current. The line in the middle of the increase signifies a wash step.

Figures 9a-9p illustrate the cDNA sequence for human mGluR2 (SEQ. ID. NO. 26), chimeric hCAR/hmGluR2 (SEQ. ID. NO. 30), chimeric hmGluR2/hCaR (SEQ. ID. NO. 34), and chimeric hmGluR8/hCaR (SEQ. ID. NO. 38).

Figures 10a-10f illustrate the amino acid sequence for human mGluR2 (SEQ. ID. NO. 27), chimeric hCAR/hmGluR2 (SEQ. ID. NO. 31), chimeric hmGluR2/hCaR (SEQ. ID. NO. 35), chimeric hmGluR8/hCaR (SEQ. ID. NO. 39).

Figures 11a-11v illustrate the cDNA sequence for the phCaR/hmGluR2*Gqi5 fusion construct (SEQ. ID. NO. 32), pmGluR2//CaR*G_{qi5} fusion construct (SEQ. ID. NO. 36), pmGluR2//CaR*G_{qi5}+3Ala linker fusion construct (SEQ. ID. NO. 46), and the mGluR8//CaR*G_{qi5} fusion construct (SEQ. ID. NO. 40).

Figures 12a-12h illustrate the amino acid sequence for the phCaR/hmGluR2*Gqi5 fusion construct (SEQ. ID. NO. 33), pmGluR2//CaR*G_{qi5} fusion construct (SEQ. ID. NO. 37), pmGluR2//CaR*G_{qi5}+3Ala linker fusion construct (SEQ. ID. NO. 47), and the mGluR8//CaR*G_{qi5} fusion construct (SEQ. ID. NO. 41).

Figures 13a-13m illustrate the cDNA sequence for the GABA-R2*Gqo5 fusion construct (SEQ. ID. NO. 42) and the GABA-BR1a*Gqo5 fusion construct (SEQ. ID. NO. 44).

Figures 14a-14e illustrates the amino acid sequence for the GABA-BR2*Gqo5 fusion construct (SEQ. ID. NO. 43) and the GABA-BR1a*Gqo5 fusion construct (SEQ. ID. NO. 45).

Figure 15 illustrates the ability of different G-protein fusions to transduce signal resulting from ligand binding. mGluR2//CaR*Gqi5 is shown by SEQ. ID. NO. 37, CaR/mGluR2*Gqi5 is shown by SEQ. ID. NO. 33, mGluR8//CaR*Gqi5 is shown by SEQ. ID. NO. 41.

Figures 16a-16e illustrates the amino acid sequence for the ph8SPmGluR4 chimeric construct (SEQ. ID. NO.48), the amino acid sequence for the phmGluR4//CaR*AAA*G α_{qi5} fusion construct (SEQ. ID. NO. 49), and the phmGluR8//CaR*AAA*G α_{qi5} fusion construct (SEQ. ID. NO. 50).

DETAILED DESCRIPTION OF THE INVENTION

The CaR, mGluR, and the GABA_BR are structurally similar in that they are each a single subunit membrane protein possessing an extracellular domain, a transmembrane domain comprising seven putative membrane spanning helices connected by three intracellular and three extracellular loops, and an intracellular carboxy-terminal domain.

5 Signal transduction is activated by the extracellular binding of an agonist. The signal is transduced to the intracellular components of the receptor causing an intracellular effect.

Signal transduction from agonist binding to an extracellular region can be modulated by compounds acting at a downstream transmembrane domain or the intracellular domain. Downstream effects include antagonist actions of compounds and
10 allosteric actions of compounds.

The transmembrane domain provides different types of target sites for compounds modulating receptor activity in different environments. As noted above, the transmembrane domain contains extracellular, transmembrane, and intracellular components.

15 Compounds modulating GABA_BR, CaR, or mGluR activity can be obtained, for example, by screening a group or library of compounds to identify those compounds having the desired activity and then synthesizing such compound. Thus, included in the present invention is a method of making a GABA_BR, CaR, or mGluR active compound by first screening for a compound having desired properties and then chemically synthesizing
20 that compound.

Metabotropic Glutamate Receptors (mGluRs)

mGluRs are G protein-coupled receptors capable of activating a variety of intracellular secondary messenger systems following the binding of glutamate (Schoepp *et al.*, *Trends Pharmacol. Sci.* 11:508, 1990; Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993, hereby incorporated by reference herein).

Activation of different mGluR subtypes *in situ* elicits one or more of the following responses: activation of phospholipase C, increases in phosphoinositide (PI) hydrolysis, intracellular calcium release, activation of phospholipase D, activation or inhibition of
30 adenylyl cyclase, increases and decreases in the formation of cyclic adenosine monophosphate (cAMP), activation of guanylyl cyclase, increases in the formation of cyclic guanosine monophosphate (cGMP), activation of phospholipase A₂, increases in arachidonic acid release, and increases or decreases in the activity of voltage- and ligand-

gated ion channels (Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993; Schoepp, *Neurochem. Int.* 24:439, 1994; Pin and Duvoisin, *Neuropharmacology* 34:1, 1995, hereby incorporated by reference herein).

Eight distinct mGluR subtypes have been isolated. (Nakanishi, *Neuron* 13:1031, 1994; Pin and Duvoisin, *Neuropharmacology* 34:1, 1995; Knopfel et al., *J. Med. Chem.* 38:1417; *Eur. J. Neuroscience* 7:622-629, 1995, each of these references is hereby incorporated by reference herein.) The different mGluRs possess a large amino-terminal extracellular domain (ECD) followed by a seven putative transmembrane domain (7TMD) comprising seven putative membrane spanning helices connected by three intracellular and three extracellular loops, and an intracellular carboxy-terminal domain of variable length (cytoplasmic tail).

Human mGluR8 is described by Stormann *et al.*, U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084, and mouse mGluR8 is described by Duvoisin *et al.*, *J. Neurosci.* 15:3075-3083, 1995, (both of these references are hereby incorporated by reference herein). mGluR8 couples to G_i. Agonists of mGluR8 include L-glutamate and L-2-amino-4-phosphonobutyrate.

mGluR8 activity can be measured using standard techniques. For example, G_i negatively couples to adenylate cyclase to inhibit intracellular cAMP accumulation in a pertussis toxin-sensitive fashion. Thus, mGluR8 activity can be measured, for example, by measuring inhibition of forskolin-stimulated cAMP production as described by Duvoisin *et al.*, *J. Neurosci.* 15:3075-3083, 1995.

mGluRs have been implicated in a variety of neurological pathologies. Examples of such pathologies include stroke, head trauma, spinal cord injury, epilepsy, ischemia, hypoglycemia, anoxia, and neurodegenerative diseases such as Alzheimer's disease (Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993; Cunningham *et al.*, *Life Sci.* 54:135, 1994; Pin et al., *Neuropharmacology* 34:1, 1995; Knopfel et al., *J. Med. Chem.* 38:1417, 1995, each of which is hereby incorporated by reference herein).

Calcium Receptor

The CaR responds to changes of extracellular calcium concentration and also responds to other divalent and trivalent cations. The CaR is a G-protein coupled receptor containing an extracellular Ca²⁺ binding domain. Activation of the CaR, descriptions of CaRs isolated from different sources, and examples of CaR active compound are provided

in Nemeth *NIPS* 10:1-5, 1995, Brown *et al.* U.S. Patent No. 5,688,938, Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, Brown E.M. *et al.*, *Nature* 366:575, 1993, Riccardi D., *et al.*, *Proc. Nat'l. Acad. Sci. USA* 92:131-135, 1995, and Garrett J.E., *et al.*, *J. Biol. Chem.* 31:12919-12925, 1995. (Each of these references are hereby incorporated by reference herein.) Brown *et al.* U.S. Patent No. 5,688,938 and Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, describe different types of compounds active at the CaR including compounds which appear to be allosteric modulators and CaR antagonists.

The CaR can be targeted to achieve therapeutic effects. Examples of target diseases are provided in Brown *et al.* U.S. Patent No. 5,688,938, and Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, and include hyperparathyroidism and osteoporosis.

γ -Aminobutyric acid Receptors (GABA_BRs)

GABA_BRs are G-protein coupled metabotropic receptors. GABA_BRs modulate synaptic transmission by inhibiting presynaptic transmitter release and by increasing K⁺ conductance responsible for long-lasting inhibitory postsynaptic potentials. (See, Kaupmann *et al.*, *Nature* 386:239-246, 1997, hereby incorporated by reference herein.)

GABA_BRs are found in the mammalian brain, in locations outside of the brain, and in lower species. Outside of the brain, GABA_BRs have been identified on axon terminals and ganglion cell bodies of the autonomic nervous system, on fallopian tube and uterine intestinal smooth muscle cells, in the kidney cortex, urinary bladder muscle and on testicular interstitial cells. (See, Bowery, *Annu. Rev. Pharmacol. Toxicol.* 33:109-147, 1993, hereby incorporated by reference herein.)

Different GABA_BRs subtypes exist. Kaupmann *et al.*, *Nature* 386:239-246, 1997, indicate that they cloned GABA_BRs. Nucleic acid encoding two GABA_BR proteins were indicated to be cloned from rat brain: GABA_BR1a and GABA_BR1b. GABA_BR1a differs from GABA_BR1b in that the N-terminal 147 residues are replaced by 18 amino acids.

GABA_BR1a and GABA_BR1b appear to be splice variants. The cloned GABA_BRs were indicated to negatively couple adenylyl cyclases and show sequence similarity to the metabotropic receptors for L-glutamate (mGluR). Northern blot analysis indicated that

GABA_BR1a and GABA_BR1b is present in brain and testis, but not in kidney, skeletal muscle, liver, lung, spleen, or heart.

Kaupmann *et al.*, International Application Number PCT/EP97/01370, International Publication Number WO 97/46675, indicate that they have obtained rat GABA_BR clones, GABA_BR1a and GABA_BR1b; and humans GABA_BR clones, GABA_BR1a/b (representing a partial receptor clone) and GABA_BR1b (representing a full-length receptor clone). Amino acid sequence information, and encoding cDNA sequence information, is provided for the different GABA_BR clones.

Another GABA_BR subtype is GABA_BR2. Northern blot analysis reveals that an approximately 6.3 Kb human GABA_BR2 transcript is abundantly expressed in the human brain. Expression is not detected in the heart, placenta, lung, liver, skeletal muscle, kidney and pancreas under conditions where GABA_BR2 transcript was identified in the human brain. Within the human brain GABA_BR2 is broadly expressed at variable levels.

GABA_BR functions as a heterodimer of the subunits GABA_BR1 or GABA_BR2. (Jones *et al. Nature* 396:674-679, 1998, hereby incorporated by reference herein.)

GABA_BRs have been targeted to achieve therapeutic effects. Kerr and Ong, DDT 1:371-380, 1996, describe different compounds indicated to be GABA_BR agonists and GABA_BR antagonists. Kerr and Ong also review therapeutic implications of affecting GABA_BR activity including, spasticity and motor control, analgesia, epilepsy, cognitive effects, psychiatric disorders, alcohol dependence and withdrawal, feeding behavior, cardiovascular and respiratory functions, and peripheral functions.

Bittiger *et al.*, *Tips* 4:391-394, 1993, review therapeutic applications of GABA_BR antagonists. Potential therapeutic applications noted by Bittiger *et al.* include cognitive processes, epilepsy, and depression.

G-Protein Fusion Receptors

Examples of some different types of G-protein fusion receptors, and advantages of some receptors, are provided below. Using the present application as guide additional G-protein receptors fusion can be constructed.

G-protein fusion receptors contain an intracellular domain of a receptor fused to a G-protein subunit (G). G fusions to adrenoreceptors have been reported by Bertin *et al.*, *Receptors and Channels* 5:41-51, 1997; Wise and Milligan, *Journal of Biological Chemistry* 39:24673-24678, 1997; and Bertin *et al.*, *Proc. Natl. Acad. Sci. USA* 91:8827-

8831, 1994 (each of which are hereby incorporated by reference herein). These studies were indicated to produce a functional chimeric by fusing the α_2 -adrenoreceptor to the G_{i1} , or the α_2 -adrenoreceptor to the G_s .

The G-protein fusion receptors described by the present invention include a G-protein fused to an intracellular domain, where the intracellular domain when present in a wild type receptor does not interact with that type of G-protein. Thus, the present invention also describes swapping of signals by fusing an intracellular domain to a G normally not coupled to that intracellular domain. The use of such fusion proteins, while applicable to chimeric GABA_BRs, is not limited to chimeric GABA_BRs. Indeed, such technology can be applied to receptors containing an extracellular domain, transmembrane domain and intracellular domain of a wild type receptor.

Preferred G-proteins fusion receptors contain an intracellular domain fused to a promiscuous G that couples to phospholipase C resulting in the mobilization of intracellular calcium. Increases in intracellular calcium can be conveniently measured through the use of dyes. Such techniques are well known in the art and are described, for example by Brown *et al.* U.S. Patent No. 5,688,938.

In an embodiment G-proteins fusions can also be used to decrease receptor desensitization.

Examples of promiscuous G's coupling to phospholipase C include naturally occurring G-proteins such as G_{15} and G_{16} , and chimeric G-protein such as Gqo5 and Gqi5. Gqo5 and Gqi5 are made of a Gq portion where the five amino acids at the C-terminal are from either G_o or G_i , respectively (Conklin *et al.*, *Nature* 363:274-277, 1993, hereby incorporated by reference herein). The Gq portion of such chimeric receptors provides for phospholipase C coupling while the terminal G_o or G_i portion allows the chimeric G-protein to couple to different receptor proteins that are normally involved in inhibitor effects on adenylate cyclase.

In an embodiment of the present invention the employed G-protein is from a human source or is made up of different G-protein components each from a human source.

G-proteins fusions can be created, for example, by fusing directly or indirectly the intracellular domain of a receptor protein to a polypeptide having an amino acid sequence substantially similar to G_{15} , G_{16} , Gqo5 or Gqi5. In different embodiments, the receptor

is fused directly or indirectly to a G-protein consisting of the amino acid sequence of G₁₅, G₁₆, Gqo5 or Gqi5.

The intracellular domain portion of a receptor protein fused directly or indirectly to a G-protein should be at least about 1 amino acid in length. In different embodiments the portion is at least about 10 amino acids, is at least about 50 amino acids, at least about 100 amino acids, or the full length of an intracellular domain.

The intracellular domain can be directly linked to a G-protein or can be indirectly linked through an optionally present linker. Optionally present linkers are preferably about 3 to about 30 amino acids in length. Preferred linkers are made up of alanine, glycine, or a combination thereof.

Chimeric Receptors

Examples of some different types of chimeric receptors, and advantages of some receptors, are provided below. Using the present application as guide additional chimeric receptors can be constructed.

Chimeric GABA_BR Extracellular Domain

Chimeric GABA_BRs containing a GABA_BR extracellular domain are particularly useful for studying the importance of the GABA_BR extracellular domain and assaying for compounds active at the extracellular domain. Preferably chimeric GABA_BRs containing a GABA_BR extracellular domain also contain a CaR intracellular domain.

A variety of different activities have been generally attributed to GABA_BR subtypes. (*E.g.*, Kerr and Ong, DDT 1:371-380, 1996.) Kaupmann *et al.*, *Nature* 386:239-246, 1997, report that in preliminary experiments involving GABA_BR1a they did not detect positive coupling to the adenylyl cyclase or coupling to the phospholipase effector system.

An intracellular CaR domain can be used to couple with G-proteins which activate phospholipase C and mobilize intracellular calcium. Mobilization of intracellular calcium is readily detected, for example, by fluorescent indicators of intracellular Ca²⁺.

An additional advantage of using the intracellular CaR domain is that CaR G-protein activation is not rapidly desensitized. Thus, the intracellular CaR domain can be used to produce a stronger intracellular signal than a signal produced from a receptor which is desensitized rapidly.

More preferably, the chimeric GABA_BR contains an intracellular CaR domain, and also contains either a CaR or a GABA_BR transmembrane domain. Advantages of using a CaR transmembrane domain include separating the effects occurring at a GABA_BR extracellular domain from effects occurring at a transmembrane domain; and providing additional intracellular elements, present on transmembrane intracellular loops, useful for coupling to G-protein.

A GABA_BR transmembrane domain is useful for examining whether the transmembrane GABA_BR can be targeted to affect GABA_BR activity, and obtaining compounds active at the GABA_BR transmembrane domain. For example, a transmembrane GABA_BR can be used to screen for transmembrane allosteric modulators and antagonists.

Chimeric GABA_BR Transmembrane Domain

Chimeric GABA_BRs containing a GABA_BR transmembrane are particularly useful for studying the importance of the GABA_BR transmembrane domain and assaying for compounds active at the transmembrane domain. Preferably Chimeric GABA_BRs containing a GABA_BR transmembrane domain contain an extracellular domain which is either mGluR8 or CaR, and an intracellular CaR domain.

More preferably, the chimeric GABA_BR contains an extracellular domain from either mGluR8 or CaR, a GABA_BR transmembrane, and an intracellular CaR domain. A chimeric GABA_BR containing extracellular mGluR8 or CaR domains can readily be stimulated using mGluR8 or CaR ligands.

Chimeric GABA_BR Intracellular Domain

Chimeric GABA_BRs containing a GABA_BR intracellular domain are particularly useful for studying the importance of the GABA_BR intracellular domain and assaying for compounds active at the intracellular domain. Preferably, the chimeric receptors contain an extracellular domain from either mGluR8 or CaR. The extracellular mGluR8 or CaR domains can readily be activated using mGluR8 or CaR ligands.

Receptor Domains

Domains of a G-protein fusion receptor, a chimeric receptor, and G , substantially similar to a particular sequence can be readily produced using the disclosure provided

herein in conjunction with information well known in the art. Substantially similar sequences can be obtained taking into account sequence information for a particular type of receptor obtained from different sources, different types of amino acids which are to some extent interchangeable, and the ease of experimentation with which functional
5 receptor activity can be assayed.

Substantially similar sequences includes amino acid alterations such as deletions, substitutions, additions, and amino acid modifications. A "deletion" refers to the absence of one or more amino acid residue(s) in the related polypeptide. An "addition" refers to the presence of one or more amino acid residue(s) in the related polypeptide. Additions
10 and deletions to a polypeptide may be at the amino terminus, the carboxy terminus, and/or internal. Amino acid "modification" refers to the alteration of a naturally occurring amino acid to produce a non-naturally occurring amino acid. A "substitution" refers to the replacement of one or more amino acid residue(s) by another amino acid residue(s) in the polypeptide. Derivatives can contain different combinations of alterations including more
15 than one alteration and different types of alterations.

The sequences of polypeptides can be compared from different sources to help identify variable amino acids not essential for receptor activity. For example, Figure 7 provides the rat GABA_BR1a and GABA_BR1b amino acid sequences. The rat GABA_BR1a and GABA_BR1b amino acid sequences can be compared with the human GABA_BR1a and
20 GABA_BR1b sequences to identify conserved and variable amino acids. Derivatives can then be produced where a variable amino acid is changed, and receptor activity can be readily tested.

Similarly, the amino acid sequences for CaR, mGluR8, and G-proteins from different sources are either known in the art or can readily be obtained. Examples of such
25 references are provided above.

While the effect of an amino acid change varies depending upon factors such as phosphorylation, glycosylation, intra-chain linkages, tertiary structure, and the role of the amino acid in the active site or a possible allosteric site, it is generally preferred that a substituted amino acid is from the same group as the amino acid being replaced. To some
30 extent the following groups contain amino acids which are interchangeable: the basic amino acids lysine, arginine, and histidine; the acidic amino acids aspartic and glutamic acids; the neutral polar amino acids serine, threonine, cysteine, glutamine, asparagine and, to a lesser extent, methionine; the nonpolar aliphatic amino acids glycine, alanine, valine,

isoleucine, and leucine (however, because of size, glycine and alanine are more closely related and valine, isoleucine and leucine are more closely related); and the aromatic amino acids phenylalanine, tryptophan, and tyrosine. In addition, although classified in different categories, alanine, glycine, and serine seem to be interchangeable to some extent, and cysteine additionally fits into this group, or may be classified with the polar neutral amino acids.

While proline is a nonpolar neutral amino acid, its replacement represents difficulties because of its effects on conformation. Thus, substitutions by or for proline are not preferred, except when the same or similar conformational results can be obtained.

The conformation conferring properties of proline residues may be obtained if one or more of these is substituted by hydroxyproline (Hyp).

Examples of modified amino acids include the following: altered neutral nonpolar amino acids such as α -amino acids of the formula $H_2N(CH_2)_nCOOH$ where n is 2-6, sarcosine (Sar), tbutylalanine (t-BuAla), t-butylglycine (t-BuGly), N-methyl isoleucine (N-MeIle), and norleucine (Nleu); altered neutral aromatic amino acids such as phenylglycine; altered polar, but neutral amino acids such as citrulline (Cit) and methionine sulfoxide (MSO); altered neutral and nonpolar amino acids such as cyclohexyl alanine (Cha); altered acidic amino acids such as cysteic acid (Cya); and altered basic amino acids such as ornithine (Orn).

Preferred derivatives have one or more amino acid alteration(s) which do not significantly affect the receptor activity of the related receptor protein. In regions of receptor domains not necessary for receptor activity, amino acids may be deleted, added or substituted with less risk of affecting activity. In regions required for receptor activity, amino acid alterations are less preferred as there is a greater risk of affecting receptor activity.

Derivatives can be produced using standard chemical techniques and recombinant nucleic acid techniques. Modifications to a specific polypeptide may be deliberate, as through site-directed mutagenesis and amino acid substitution during solid-phase synthesis, or may be accidental such as through mutations in hosts which produce the polypeptide. Polypeptides including derivatives can be obtained using standard techniques such as those described by Sambrook *et al.*, *Molecular Cloning*, Cold Spring Harbor Laboratory Press (1989). For example, Chapter 15 of Sambrook describes procedures for site-directed mutagenesis of cloned DNA.

Receptor Nucleic Acid

G-protein fusion and chimeric receptor nucleic acid can be produced based on the information provided herein along with standard recombinant nucleic acid techniques.

5 Examples of references describing recombinant nucleic acid techniques include *Molecular Cloning*, Sambrook *et al.*, Cold Spring Harbor Laboratory Press (1989); and *Current Protocols in Molecular Biology*, Frederick *et al.*, John Wiley & Sons, Inc. (1995).

10 Due to the degeneracy of the genetic code different nucleic acid sequences can encode for a particular polypeptide. Thus, a large number of nucleic acids encoding for a receptor having the same amino acid sequence can be produced.

An embodiment of the present invention uses human nucleic acid encoding for the domains from CaR, GABA_BR1A, GABA_BR1B, GABA_BR2 and/or mGluR8. The amino acid sequences of different domains is provided in Figures 1-3.

Recombinant Cells

15 Nucleic acid expressing a functional G-Protein fusion or a chimeric receptor can be used to create transfected cells lines expressing such receptors. Such cell lines have a variety of uses such as being used for high-throughput screening for compounds modulating receptor activity; being used to assay binding to the receptor; and as factories to produce large amounts of a receptor.

20 A variety of cell lines can couple exogenously expressed receptors to endogenous functional responses. Cell lines such as NIH-3T3, HeLa, NG115, CHO, HEK 293 and COS7 which are expected to lack CaR, mGluR8, and GABA_BR can be tested to confirm that they lack these receptors.

25 Production of stable transfectants can be accomplished by transfection of an appropriate cell line with, for example, an expression vector such as pMSG vector, in which the coding sequence for the G-protein fusion or chimeric GABA_BR cDNA has been cloned. Expression vectors containing a promoter region, such as the mouse mammary tumor virus promoter (MMTV), drive high-level transcription of cDNAs in a variety of mammalian cells. In addition, these vectors contain genes for selecting cells stably expressing cDNA of interest. The selectable marker in the pMSG vectors encode an

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enzyme, xanthine-guanine phosphoribosyl transferase (XGPRT), conferring resistance to a metabolic inhibitor that is added to the culture to kill nontransfected cells.

The most effective method for transfection of eukaryotic cell lines with plasmid DNA varies with the given cell type. The expression construct will be introduced into cultured cells by the appropriate technique, such as Ca^{2+} phosphate precipitation, DEAE-dextran transfection, lipofection or electroporation. Expression of the receptor cDNA in cell lines can be assessed by solution hybridization and Northern blot analysis.

Binding Assays

The present invention also includes using G-protein fusion receptors or chimeric GABA_BR in a binding assay. G-protein fusion receptors or chimeric GABA_BRs having a particular GABA_BR domain can be used, for example to facilitate obtaining compounds able to bind to that particular receptor domain; and to determine whether a compound which binds to a particular domain. For example, in a complete chimeric GABA_BR containing extracellular, transmembrane, and intracellular domains, the presence of one or more domains from CaR or mGluR are useful to present GABA_BR domain(s) to a binding agent in a form more like the GABA_BR domain(s) in the wild type receptor compared to an incomplete GABA_BR receptor fragment lacking one or more domains.

Binding assays can be carried out using techniques well known in the art. Binding assays preferably employ radiolabeled binding agents.

An example of a binding procedure is carried out by first attaching chimeric GABA_BR to a solid-phase support to create an affinity matrix. The affinity matrix is then contacted with potential GABA_BR binding agents. A large library of compounds may be used to determine those compounds binding to the affinity matrix. Bound compounds can be eluted from the column.

Therapeutic Modulation

As pointed out above, different types of diseases and disorders can be treated using compounds modulating CaR, mGluR, or GABA_BR activity. Additionally, such compounds can be used prophylactically. Compounds modulating $\text{GABA}_B\text{R2}$ activity can be administered to patients who would benefit from such treatment. Patients are mammals, preferably humans.

Modulators of CaR, mGluR, or GABA_BR activity can be administered to a patient using standard techniques. Techniques and formulations generally may be found in Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, 1990 (hereby incorporated by reference herein).

5 Suitable dosage forms, in part, depend upon the use or the route of entry, for example, oral, transdermal, transmucosal, or by injection (parenteral). Such dosage forms should allow the therapeutic agent to reach a target cell whether the target cell is present in a multicellular host or in culture. For example, pharmacological compounds or compositions injected into the blood stream should be soluble. Other factors are well
10 known in the art, and include considerations such as toxicity and dosage forms which retard the therapeutic agent from exerting its effect.

Therapeutic compounds can be formulated as pharmaceutically acceptable salts and complexes thereof. Pharmaceutically acceptable salts are non-toxic salts in the amounts and concentrations at which they are administered. The preparation of such salts
15 can facilitate the pharmacological use by altering the physical characteristics of the compound without preventing it from exerting its physiological effect. Useful alterations in physical properties include lowering the melting point to facilitate transmucosal administration and increasing the solubility to facilitate administering higher concentrations of the drug.

20 The pharmaceutically acceptable salt of a compound may be present as a complex. Examples of complexes include an 8-chlorotheophylline complex (analogous to, *e.g.*, dimenhydrinate:diphenhydramine 8-chlorotheophylline (1:1) complex; Dramamine) and various cyclodextrin inclusion complexes.

Pharmaceutically acceptable salts include acid addition salts such as those
25 containing sulfate, hydrochloride, fumarate, maleate, phosphate, sulfamate, acetate, citrate, lactate, tartrate, methanesulfonate, ethanesulfonate, benzenesulfonate, *p*-toluenesulfonate, cyclohexylsulfamate and quinate.

Pharmaceutically acceptable salts can be obtained from acids such as hydrochloric acid, maleic acid, sulfuric acid, phosphoric acid, sulfamic acid, acetic acid, citric acid,
30 lactic acid, tartaric acid, malonic acid, methanesulfonic acid, ethanesulfonic acid, benzenesulfonic acid, *p*-toluenesulfonic acid, cyclohexylsulfamic acid, fumaric acid, and quinic acid.

Pharmaceutically acceptable salts also include basic addition salts such as those containing benzathine, chlorprocaine, choline, diethanolamine, ethylenediamine, meglumine, procaine, aluminum, calcium, lithium, magnesium, potassium, sodium, ammonium, alkylamine, and zinc, when acidic functional groups, such as carboxylic acid or phenol are present. For example, see Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, p. 1445, 1990. Such salts can be prepared using the appropriate corresponding bases.

Carriers or excipients can also be used to facilitate administration of therapeutic agents. Examples of carriers include calcium carbonate, calcium phosphate, various sugars such as lactose, glucose, or sucrose, or types of starch, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols and physiologically compatible solvents. Examples of physiologically compatible solvents include sterile solutions of water for injection (WFI), saline solution and dextrose.

GABA_BR modulating compounds can be administered by different routes including intravenous, intraperitoneal, subcutaneous, intramuscular, oral, topical (transdermal), or transmucosal administration. For systemic administration, oral administration is preferred. For oral administration, for example, the compounds can be formulated into conventional oral dosage forms such as capsules, tablets, and liquid preparations such as syrups, elixirs, and concentrated drops.

Alternatively, injection (parenteral administration) may be used, *e.g.*, intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, compounds are formulated in liquid solutions, preferably, in physiologically compatible buffers or solutions, such as saline solution, Hank's solution, or Ringer's solution. In addition, the compounds may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms can also be produced.

Systemic administration can be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are well known in the art, and include, for example, for transmucosal administration, bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration, for example, may be through nasal sprays, rectal suppositories, or vaginal suppositories.

For topical administration, compounds can be formulated into ointments, salves, gels, or creams, as is well known in the art.

The amounts of various GABA_BR modulating compounds to be administered can be determined by standard procedures taking into account factors such as the compound
5 IC₅₀, EC₅₀, the biological half-life of the compound, the age, size and weight of the patient, and the disease or disorder associated with the patient. The importance of these and other factors to be considered are well known to those of ordinary skill in the art. Generally, the amount is expected to preferably be between about 0.01 and 50 mg/kg of the animal to be treated.

10

EXAMPLES

Examples are provided below illustrating different aspects and embodiments of the present invention. The examples include techniques that can be used to produce and use G-protein fusion receptors and chimeric receptors. These examples are not intended to
15 limit the claimed invention.

Example 1: Construction of G-Protein Fusions

This example illustrates different G-protein fusion receptor constructs and techniques used to produce different G-protein fusion receptor constructs. Numbering of
20 nucleotide position for all the following constructs is such that nucleotide number 1 corresponds to the A of the ATG start codon of the nucleotide sequence encoding the designated protein.

I. FULL-LENGTH CONSTRUCTS

A. phCaR

The cDNA encoding the human CaR (Garrett et al., (1995) J. Biol. Chem.270:12919) is harbored in the Bluescript SK(-) plasmid (Stratagene). This construct is referred to as phCaR.

B. phmGluR2

A full length human mGluR2 cDNA was amplified from human cerebellum MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR2 cDNA sequence (Genbank Accession # 4504136). The obtained PCR fragment was

subcloned into the pT7Blue TA vector (Novagen). A Hind III-Not I fragment containing the human mGluR2 cDNA was then subcloned into the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phmGluR2.

5 C. phGα_q

A full length human Gα_q cDNA was amplified from human cerebral cortex Quick-Clone cDNA (Clontech) using PCR primers based on the human Gα_q cDNA sequence (Genbank Accession # 4504044). The obtained PCR fragment was subcloned into the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phGα_q.

10 D. phmGluR8

The cDNA encoding the full length human mGluR8 cDNA (Stormann *et al.*, U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084) is harbored in the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phmGluR8.

15 E. ph8SPmGluR4

A full length human mGluR4 cDNA was amplified from human cerebellum MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR4 cDNA sequence (Genbank Accession #X80818). The obtained PCR fragment was cloned into the pT7Blue TA vector (Novagen). A 2977 bp BamHI fragment containing the human mGluR4 cDNA was then subcloned into the vector pcDNA3.1/Hygro⁺ (Invitrogen). This construct is referred to as phmGluR4.

Next, the predicted signal peptide of mGluR4 was replaced with the predicted signal peptide and 87 bp of 5' UTR from phmGluR8 using a recombinant PCR strategy similar to those described above. The first reaction used a phmGluR8 construct with two primers, 3.1-535F (sense 21-mer, complementary to vector sequence upstream of the hmGluR8 insert; sequence 5'-ggcattatgccagtagcatga-3'), and the hybrid primer 8/4RP (antisense 42-mer, containing 21 nucleotides complementary to human mGluR8 and 21 nucleotides complementary human mGluR4; sequence 5'-caagcctctcttcccaggttttccacaggtgtattgc-3'). These primers were used to amplify a 469 bp PCR fragment of human mGluR8.

In a separate PCR reaction using phmGluR4 as template, a 472 bp fragment of

human mGluR4 was amplified using a hybrid primer 4/8RP (sense 42-mer, exactly complementary to primer 8/4RP) and oligo mG4-472R, (antisense 18-mer, complementary to the human mGluR4 cDNA; sequence 5'-ctgaagcaccgatgacac-3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers mG4-472R and 3.1-535F, and Turbo Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with NarI and NheI (New England Biolabs) and subcloned into phmGluR4 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, ph8SPmGluR4, was verified by ABI automated DNA sequence analysis. The replacement of the predicted signal peptide of mGluR4 with that of mGluR8 greatly increased the activity of this receptor in *in vitro* assays

II. G α q15

The cDNA encoding the human G α q15 cDNA (Conklin et al (1993) Nature 363:274-77) is harbored in the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as G α q15. The nucleic acid and amino acid sequences for G α q15 are provided by SEQ. ID. NOs. 28 and 29 respectively.

III. phCaR/hmGluR2

This chimera contains the extracellular domain of the human CaR and transmembrane domain and intracellular cytoplasmic tail of human mGluR2. The chimeric junction between the CaR and hmGluR2 was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, CA1156 (sense 19-mer, corresponding to nucleotides 1156-1174 of human CaR), and the hybrid primer CA/2 (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 1774-1794 of human CaR and 21 nucleotides complementary to nucleotides 1660-1680 of the human mGluR2). These primers were used to amplify a 659 bp PCR fragment of human CaR.

In a separate PCR reaction using phmGluR2 as template, a 692 bp fragment of the human mGluR2 was amplified using a hybrid primer 2/CA (sense 42-mer, exactly complementary to primer CA/2) and oligo 2-2330m, (antisense 23-mer, complementary to

nucleotides 2309-2331 of the human mGluR2 cDNA). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CA1156 and 2-2330m, and the Pfu DNA polymerase (Stratagene).

5 The resulting chimeric PCR product was digested with SexA1 (Boehringer Mannheim) and BamHI (New England Biolabs) and subcloned into phCaR digested with the same two restriction enzymes. In the final cloning step, the 3' end of human mGluR2 was subcloned into this construct using the restriction enzymes BsrGI and BamHI (both New England Biolabs). The sequence of the resultant chimeric construct,
10 phCaR/hmGluR2, was verified by ABI automated DNA sequence analysis.

IV. phCaR/hmGluR2*Gqi5

This construct contains the phCaR/hmGluR2 chimeric receptor fused to human $G\alpha_{qi5}$. A HindIII-BamHI fragment containing the phCaR/hmGluR2 construct was
15 subcloned into pcDNA3.1/Hygro(+) (Invitrogen) to aid in constructing this fusion protein.

The chimeric junction between the C-terminus of phCaR/hmGluR2 and the N-terminus of $G\alpha_{qi5}$ was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, 2-1713 (sense 21-mer, corresponding to
20 nucleotides 1710-1730 of human mGluR2) and the hybrid primer 2/Q (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 2596-2616 of human mGluR2, and 21 nucleotides complementary to nucleotides 1-21 of p $G\alpha_{qi5}$). These primers were used to amplify a 927 bp PCR fragment of phCaR/hmGluR2. In a separate PCR reaction all of $G\alpha_{qi5}$ was amplified using a hybrid primer Q/2 (sense 42-mer, exactly
25 complementary to primer 2/Q) and the and the T3 primer commercially available from Stratagene.

These two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 2-1713 and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested
30 with Bsu361 and BamHI (New England Biolabs) and subcloned into phCaR/hmGluR2 digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, phCaR/hmGluR2* $G\alpha_{qi5}$, was verified by DNA sequence analysis.

V. phmGluR2//CaR Construct

This chimera contains the extracellular and transmembrane domains of human mGluR2 linked to the intracellular cytoplasmic tail domain of the human CaR. The chimeric junction was created using three separate PCR reactions.

The first reaction used two primers, 2-1713 (sense 21-mer, corresponding to nucleotides 1710-1730 of human mGluR2, Genbank Accession # 4504136) and the hybrid primer 2/CT (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 2452 – 2472 of human mGluR2 and 21 nucleotides complementary to nucleotides 2602-2622 of the human CaR). These primers were used to amplify a 783 bp PCR fragment of human mGluR2. In a separate PCR reaction using phCaR in the BlueScript SK⁻ plasmid as template, a 750 bp fragment of the human CaR was amplified using a hybrid primer CT/2 (sense 42-mer, exactly complementary to primer 2/CT) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 2-1713 and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BsrG I and Not I (New England Biolabs) and subcloned into pmGluR2 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, pmGluR2//CaR, was verified by ABI automated DNA sequence analysis.

VI. pmGluR2//CaR*Gα_qi5 Construct

This construct contains the hmGluR2//CaR chimeric receptor fused to human Gα_qi5. The chimeric junction between the C-terminus of hmGluR2//CaR and the N-terminus of Gα_qi5 was created using a recombinant PCR strategy similar to that described above for the construction of phmGluR2//CaR.

The first reaction used two primers, CRP10A (sense 18-mer, corresponding to nucleotides 2812-2829 of phCaR) and the hybrid primer CaRQ (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 3214– 3234 phCaR, and 21 nucleotides complementary to nucleotides 1-21 of pGα_qi5). These primers were used to amplify a 443 bp PCR fragment of hmGluR2//CaR. In a separate PCR reaction, all of Gα_qi5 was amplified using a hybrid primer QCaR (sense 42-mer, exactly complementary

to primer CaRQ) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CRP10A and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BstE II and Not I (New England Biolabs) and subcloned into pmGluR2//CaR
 5 digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, pmGluR2//CaR*G α _qi5, was verified by ABI automated DNA sequence analysis.

VII. Fusion Receptor Protein Linker Addition Constructs

A. phmGluR2//CaR*AAA*G α _qi5

A linker encoding three alanine residues was incorporated into the phmGluR2//CaR*G α _qi5 construct by mutagenesis (Stratagene QuickChange Mutagenesis
 15 Kit). A sense 40-mer, 2CQ+LP, contained 16 nucleotides corresponding to 3219-3234 of human CaR, followed by the 9 nucleotide sequence (GCGGCCGCC) encoding three alanine residues and a NotI restriction enzyme site, and then 15 nucleotides corresponding to nucleotides 1-15 of G α _qi5. 2CQ+LP was annealed to an antisense 40-mer, 2CQ+LM, the exact complement of 2CQ+LP. These oligos were used in the mutagenesis reaction
 20 according to the manufacturer's protocol. Restriction enzyme analysis and DNA sequence analysis confirmed the insertion of the 9 nucleotide linker (GCGGCCGCC) between the C-terminus of phmGluR2//CaR and the N-terminus of G α _qi5. This construct was designated phmGluR2//CaR*AAA*G α _qi5.

B. Human GABA_BR2*AAA*G α _qo5 and human GABA_BR1a*AAA*G α _qo5

These constructs contain the human GABA_BR2 (hGABA_BR2: Genbank Accession # AJ 012188) and human GABA_BR1a (hGABA_BR1a: Genbank Accession # AJ 012185) fused at their C-terminus to the N-terminus of human G α _qo5 (hG α _qo5: *Nature* 363:274-276, 1993). Human GABA_BR2, hGABA_BR1a, and hG α _qo5 were cloned into the plasmid
 30 pcDNA3.1/Hygro+ (Invitrogen) and are designated phGABA_BR2, phGABA_BR1a, and phG α _qo5. The first reaction used two primers, XcmI-R2 (sense 20-mer, corresponding to nucleotides 2650-2669 of phGABA_BR2) and the hybrid primer R2/Go5(-) (antisense 45-

mer, containing 18 nucleotides complementary to nucleotides 2806-2823 of phGABA_BR2 and 18 nucleotides complementary to nucleotides 1-18 of hGα_qo5). These two complementary areas flank a 9 nucleotide sequence coding for 3 alanine sequences with a unique NotI restriction site. These primers were used to amplify a 200 base-pair PCR
 5 fragment.

In a separate PCR reaction, part of hGα_qo5 was amplified using a hybrid primer R2/Gα_qo5(+) (sense 45-mer), exactly complementary to R2/Go5(-) and XbaI-Go5 primer (22-mer containing 22 nucleotides complementary to nucleotides 873-895 of hGα_qo5). These primers were used to amplify a 914 base-pair PCR product. The two PCR products
 10 generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers; XcmI-R2 and XbaI-Go5, and Pfu polymerase (Stratagene).

The resulting chimeric PCR product was digested with the restriction endonucleases XcmI and XbaI (New England Biolabs) and subcloned into phGABA_BR2 digested with the same two restriction enzymes. The resulting clone was then digested
 15 with HindIII and XbaI and subcloned into phGα_qo5 cut with HindIII and XbaI resulting in the chimeric hGABA_BR*AAA*Gα_qo5. The chimeric junction between the C-terminus hGABA_BR1a, the Ala linker, and the N-terminus of hGα_qo5 was created using a recombinant PCR strategy similar to those described above.

To construct hGABA_BR1a*AAA*Gqo5, the first reaction used a commercially available T7 primer (Novagen) and the Ntl hGBR1 primer
 20 (CAGAGTCATGGCGGCCGCCTTATAAAGCAAATGCACTCG) corresponding to nucleotide numbers 1-9 of hGα_qo5 and nucleotide numbers 2863-2883 of hGABA_BR1a.

25 C. phmGluR8//CaR*AAA*Gα_qi5

A linker encoding three alanine residues was incorporated into the phmGluR8//CaR*Gα_qi5 construct by mutagenesis (Stratagene QuickChange Mutagenesis Kit), exactly as described in Section A, above to create phmGluR2//CaR*AAA*Gα_qi5. The same primers, 2CQ+LP and 2CQ+LM, were used for this mutagenesis. Restriction
 30 enzyme analysis and DNA sequence analysis confirmed the insertion of the 9-nucleotide linker (GCGGCCGCC) between the C-terminus of phmGluR8//CaR and the N-terminus of Gα_qi5. This construct was designated phmGluR8//CaR*AAA*Gα_qi5.

D. ph8SPmGluR4//CaR*AAA*G α _qi5

This chimera contains the extracellular and transmembrane domains of the human 8SPmGluR4 construct and intracellular cytoplasmic tail of human CaR fused to G α _qi5 through the three alanine residue linker.

The chimeric junction between the human 8SPmGluR4 and hCaR was created using a recombinant PCR strategy similar to those previously described. The first reaction used two primers, mG4-2028R (sense 19-mer, corresponding to nucleotides of human 8SPmGluR4; sequence 5'-catctaccgcatcttcgag-3'), and the hybrid primer 4CT (antisense 42-mer, containing 21 nucleotides complementary to human 8SPmGluR4 and 21 nucleotides complementary human CaR; sequence 5'-acgcacctcctcgatgggtgttctgctccgggtggaaggagat-3'). These primers were used to amplify a 549 bp PCR fragment from human 8SPmGluR4.

In a separate PCR reaction, using phmGluR2//CaR*AAA*G α _qi5 as a template, a 743 bp fragment of the human CaR*AAA*G α _qi5 was amplified using the hybrid primer CT4 (sense 42-mer, exactly complementary to primer 4CT) and oligo G α _qi58R, (antisense 21-mer, complementary to G α _qi5 cDNA; sequence 5'-ctcgatctcgtcgttgatccg-3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers mG4-2028R and G α _qi58R, and Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested sequentially with KpnI and NotI (New England Biolabs) and subcloned into ph8SPmGluR4 prepared with the same two restriction enzymes. This intermediate construct was known as ph8SPmGluR4//CaR(no stop). In the final cloning step, a fragment containing the G α _qi5 cDNA was released from phmGluR8//CaR*AAA*G α _qi5 using the restriction enzymes ApaI and NotI (both New England Biolabs) and subcloned into the ph8SPmGluR4//CaR(no stop) construct, which was prepared with the same restriction enzymes. The sequence of the resultant chimeric construct, ph8SPmGluR4//CaR*AAA*G α _qi5, was verified by ABI automated DNA sequence analysis.

VIII. phmGluR8//CaR Construct

This chimera contains the extracellular and transmembrane domains of human mGluR8 linked to the intracellular cytoplasmic tail domain of the human CaR. The

chimeric junction between hmGluR8 and the CaR was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, CH5A (sense 19-mer, corresponding to nucleotides 2187-2205 of human mGluR8, Stormann *et al.*, U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084) and the hybrid primer CH5B (antisense 40-mer, containing 22 nucleotides complementary to nucleotides 2523 – 2544 of human mGluR8, and 18 nucleotides complementary to nucleotides 2602-2619 of the human CaR). These primers were used to amplify a 375 bp PCR fragment of human mGluR8. In a separate PCR reaction using phCaR in the BlueScript SK(-) plasmid as template, a 750 bp fragment of the human CaR was amplified using a hybrid primer CH5C (sense 40-mer, exactly complementary to primer CH5B) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CH5A and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BsrG I and Xba I (New England Biolabs) and subcloned into pmGluR8 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, pmGluR8//CaR, was verified by DNA sequence analysis.

IX. mGluR8//CaR*Gα_qi5 Construct

This construct contains the hmGluR8//CaR chimeric receptor fused to human Gα_qi5. The chimeric junction between the C-terminus of hmGluR8//CaR and the N-terminus of Gα_qi5 was created using a recombinant PCR strategy similar to that described above for the construction of phmGluR2//CaR*Gα_qi5.

The first reaction used two primers, CRP10A (sense 18-mer, corresponding to nucleotides 2812-2829 of phCaR) and the hybrid primer Gqi5/CaR (antisense 40-mer, containing 21 nucleotides complementary to nucleotides 3214-3234 phCaR, and 19 nucleotides complementary to nucleotides 1-19 of pGα_qi5). These primers were used to amplify a 441 bp PCR fragment of hmGluR8//CaR.

In a separate PCR reaction all of Gα_qi5 was amplified using a hybrid primer CaR/Gqi5 (sense 40-mer, exactly complementary to primer Gqi5/CaR) and the Apa I-mut primer (20-mer). The two PCR products generated from the above two reactions were

annealed together in equimolar ratios in the presence of the external primers CRP10A and Apa I-mut, and the Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with BstE II and Apa I (New England Biolabs) and subcloned into pmGluR8//CaR digested with the same two
 5 restriction enzymes. The sequence of the resultant chimeric fusion construct, pmGluR8//CaR*G α qi5, was verified by DNA sequence analysis.

Example 2: Functional Expression of CaR/GABA_BR2

In vitro transcribed RNA (7 ng) encoding a chimeric CaR/GABA_BR2 (CaR
 10 extracellular and transmembrane domains, and intracellular GABA_BR2 domain) was co-injected with *in vitro* transcribed RNA (2 ng) encoding G 15 into *Xenopus* oocytes. Following a 72-hour incubation, the oocytes were voltage-clamped using standard electrophysiological techniques (Hille, B., Ionic Channels of Excitable Membranes, pp.30-33, Sinauer Associates, Inc., Sunderland, Ma., 1992). Activation of the chimeric
 15 receptor was detected by increases in the calcium-activated chloride current.

Application of the CaR activator 100 Gd³⁺, resulted in reversible, oscillatory increases in the calcium-activated chloride current as shown in Figure 8. These data demonstrate the functional response of the chimeric CaR/GABA_BR2 receptor upon
 20 activation via a site within the CaR extracellular domain. In this assay, the G 15 subunit acts to promote signal transduction through intracellular pathways that mobilize intracellular Ca⁺⁺.

Example 3: Expression of Different G-Protein Fusion Receptors

The ability of different G-protein fusions to transduce signal resulting from ligand
 25 binding is shown in Figure 15. The different G-protein fusion receptors used in this example were as follows: mGluR2//CaR*Gqi5 (SEQ. ID. NO. 37), CaR/mGluR2*Gqi5 (SEQ. ID. NO. 33), and mGluR8//CaR*Gqi5 SEQ. ID. NO. 41.

Oocytes suitable for injection were obtained from adult female *Xenopus laevis* toads using procedures described in C. J. Marcus-Sekura and M. J. M. Hitchcock,
 30 Methods in Enzymology, Vol. 152 (1987).

Receptor fusion cRNAs were dissolved in water and 50 nl (12.5 ng/oocyte) were injected into individual oocytes. Following injection, oocytes were incubated at 16°C in MBS containing 1 mM CaCl₂ for 2 to 7 days prior to electrophysiological recording.

Test substances were applied by superfusion at a flow rate of about 5 ml/min. Receptor fusion activation was determined by measuring the increase in calcium-activated chloride current (I_{Cl}). Increases in I_{Cl} were quantified by measuring the peak inward current stimulated by activating agent, relative to the holding current at -60 mV.

- 5 Application of 100 μ M L-glutamate elicited a response from the mGluR2//CaR*G α q5 and mGluR8//CaR*G α q5. Application of 100 μ M Gd³⁺ activated the CaR/mGluR2*Gq5.

Example 4: Expression of Different G-Protein Fusion Receptors in Mammalian Cells

10

HEK293 cells were transiently transfected with the p8SPhmGluR4//CaR*AAA*G α q5 or phmGluR8//CaR*G α q5 plasmid DNAs using the following protocol. Initially, 150 cm² tissue culture flasks containing HEK293 cells at 75% confluence were transfected with 24 μ g of plasmid DNA using Gibco BRL Life Technologies' Lipofectamine reagent. Following liposomal gene delivery the cells were
15 allowed to recover for 24 hours. They were then plated overnight at 100,000 cells per well in black, clear bottom, Collagen I coated 96-well plates (Becton Dickinson, Biocoat) using DMEM supplemented with 10% fetal bovine serum (Hyclone Laboratories). The cells were assayed for function 48 hours after transient transfection.

20

On the day of the assay, tissue culture medium was aspirated from the wells of a 96-well plate and 80 μ L of Assay Buffer (Assay Buffer is: 20 mM HEPES, 146 mM NaCl, 5 mM KCl, 1 mM MgCl₂, 1 mM CaCl₂, 1 mg/ml BSA, 1 mg/ml glucose, pH 7.4) supplemented with 6 μ M of the Ca²⁺-sensitive dye, Fluo-3 AM (Molecular Probes) and 0.025% Pluronic (Molecular Probes) was added to each well.

25

The plate was then incubated in the dark for 1 hour at room temperature to efficiently load the cells with Fluo-3. At the end of the incubation, extracellular Fluo-3 was removed by washing the plate with Assay Buffer. Assay Buffer was added back to each well (final volume = 160 μ L) prior to beginning the assay. The plate was loaded into a fluorescence imaging plate reader (FLIPR) robotic device (Molecular Devices) with the
30 laser setting at 0.8 Watts. At a time of 15 seconds after initiation of the assay, 40 μ L of Assay Buffer containing 150 μ M L-AP4 was added to the 160 μ L of Assay Buffer in each well of the plate to yield a final concentration of 30 μ M L-AP4.

Relative fluorescence intensity (excitation $\lambda = 488$ nm / emission $\lambda = 510$ nm) was monitored at relevant time intervals throughout the assay period to measure L-AP4-induced receptor activation.

- 5 Other embodiments are within the following claims. Thus, while several embodiments have been shown and described, various modifications may be made, without departing from the spirit and scope of the present invention.

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2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2

Claims

1. A G-protein fusion receptor comprising

an extracellular domain comprising an extracellular domain amino acid sequence

substantially similar to either an extracellular CaR amino acid sequence, an extracellular mGluR amino acid sequence, or an extracellular GABA_B receptor amino acid sequence;

a transmembrane domain joined to the carboxy terminus of said extracellular domain, said transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to either a transmembrane CaR amino acid sequence, a transmembrane mGluR amino acid sequence, or a transmembrane GABA_B receptor amino acid sequence;

an intracellular domain joined to the carboxy terminus of said transmembrane domain comprising all or a portion of an intracellular amino acid sequence substantially similar to either an intracellular CaR amino acid sequence, an intracellular mGluR amino acid sequence, or an intracellular GABA_B receptor amino acid sequence, provided that said portion is at least about 10 amino acids;

an optionally present linker joined to the carboxy terminus of said intracellular domain; and

a G-protein joined either to said intracellular domain or to said optionally present linker, provided that said G-protein is joined to said optionally present linker when said optionally present linker is present.

2. The G-protein fusion receptor of claim 1, wherein said extracellular domain consists of said extracellular domain amino acid sequence, said transmembrane domain consists of said transmembrane domain amino acid sequence; and said intracellular domain consists of said transmembrane domain amino acid sequence.

3. The G-protein fusion receptor of claim 2, wherein said optionally present linker is present and is a polypeptide 3 to 30 amino acids in length.

4. The G-protein fusion receptor of claim 2, wherein said optionally present linker is not present.

5. 1. The G-protein fusion receptor of claim 3 or 4, wherein said G-protein is selected from the group consisting of: G₁₅, G₁₆, Gqo5, and Gqi5

6. The G-protein fusion of claim 5, wherein any of said CaR sequence present is a human CaR sequence, any of said mGluR sequence present is from a human mGluR, and any of said GABA_B receptor sequence present is from human mGluR.

7. A nucleic acid comprising a nucleotide sequence encoding for the G-protein fusion of any one of claims 1-6.

8. An expression vector comprising a nucleotide sequence encoding for the G-protein fusion of any one of claims 1-6 transcriptionally coupled to a promoter.

9. A recombinant cell comprising the expression vector of claim 8 and a cell wherein the G-protein fusion is expressed and is functional.

10. A recombinant cell produced by combining a vector comprising the nucleic acid of claim 9 and elements for introducing heterologous nucleic acid into a cell wherein the G-protein fusion receptor is expressed, and said cell.

11. A process for the production of a G-protein fusion receptor comprising: growing procaryotic or eukaryotic host cells comprising a nucleic acid sequence expressing the G-protein fusion receptor of any one of claims 1-6, under suitable nutrient conditions allowing for cell growth.

12. A method of measuring the ability of a compound to effect G-protein fusion activity comprising the steps of:

a) providing said compound to a cell expressing the G-protein fusion receptor of any one of claims 1-6, and

b) measuring the ability of said compound to affect the activity of said receptor as an indication of the ability of said compound to effect G-protein fusion receptor activity.

13. A chimeric receptor comprising

an extracellular domain comprising an extracellular domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 5;

a transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, and SEQ ID NO: 10; and

an intracellular cytoplasmic domain comprising an intracellular domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14;

wherein at least one domain is present which comprises an amino acid sequence substantially similar to a sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14; and at least one domain is present which comprises an amino acid sequence substantially similar to a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 11, and SEQ ID NO: 15.

14. The chimeric receptor of claim 13 wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 3, and 4; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 6, 7, 8, 9, and 10; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 11 and 15.

15. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 2; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 11.

16. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 3; said

transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

5 17. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence SEQ ID NO: 4; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

10 18. The chimeric receptor of claim 13, wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4 and 5; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 7, 8, and 9; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 12, 13, 14, and 15.

15 19. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 11.

20 20. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

25 21. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid

30

sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

22. The chimeric receptor of claim 13, wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4, and 5; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 6, 7, 8, 9, and 10; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 12, 13, and 14.

23. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 12.

24. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 12.

25. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 13.

26. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid

sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 13.

27. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 14.

28. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 14.

29. The chimeric receptor of any one of claims 13-28, wherein said receptor functional couples to a G-protein.

30. The chimeric receptor of any one of claims 13-28, wherein said chimeric receptor consists of said extracellular domain, said transmembrane domain, said intracellular domain, and an optionally present G-protein α subunit covalently joined to said intracellular domain.

31. The chimeric receptor of claim 30, wherein said chimeric receptor consists of said extracellular domain, said transmembrane domain, and said intracellular domain.

32. The chimeric receptor of claim 30, wherein said G-protein α subunit consists of the amino acid sequence of SEQ ID Nos: 16 or 17.

33. A nucleic acid comprising a nucleotide sequence encoding for the chimeric receptor of any one of claims 13-32.

34. An expression vector comprising a nucleotide sequence encoding for the chimeric receptor of any one of claims 13-32 transcriptionally coupled to a promoter.

35. A recombinant cell comprising the expression vector of claim 34 and a cell wherein the chimeric receptor is expressed and is functional.

36. A recombinant cell produced by combining a vector comprising the nucleic acid of claim 33 and elements for introducing heterologous nucleic acid into a cell wherein the chimeric receptor is expressed, and said cell.

37. A process for the production of a chimeric receptor comprising:
growing procaryotic or eukaryotic host cells comprising a nucleic acid sequence expressing the chimeric receptor of any one of claims 13-32, under suitable nutrient conditions allowing for cell growth.

38. A method of measuring the ability of a compound to effect GABA_BR or mGluR activity comprising the steps of:

a) providing said compound to a cell expressing the chimeric receptor of any one of claims 13-32, and

b) measuring the ability of said compound to affect the activity of said receptor as an indication of the ability of said compound to effect GABA_BR or mGluR activity.

39. The method of claim 38, wherein said method measures activity at a GABA_BR.

40. The method of claim 38, wherein said method measures activity at a mGluR.

41. A fusion receptor polypeptide comprising a receptor and a G-protein α subunit, wherein said G-protein α subunit is fused to the intracellular domain of said receptor, provided that said receptor is not an adrenoreceptor.

ABSTRACT

The present invention features G-protein fusion receptors and chimeric GABA_B receptors (GABA_BRs), nucleic acid encoding such receptors, and the use of such receptors and nucleic acid. G-protein fusion receptors comprise at least one domain from a CaR, a mGluR, and/or a GABA_B receptor fused directly or through a linker to a guanine nucleotide-binding protein (G-protein). Chimeric GABA_BRs comprise at least one of a GABA_BR extracellular domain, a GABA_BR transmembrane domain, or a GABA_BR intracellular domain and one or more domains from a mGluR subtype 8 (mGluR8) and/or a CaR.

ClustalW Formatted Alignments

SEQ ID 1 MAFYSCCWVLLALTWHTSAYGPDQR
 SEQ ID 2 MLLLLLLAPLFLRPPGAGGAQTPNA
 SEQ ID 3 MGPGAPFARVGVWPLPLLVMAGVA
 SEQ ID 4 MASPRSSGQPGXP PPPPPARLLL
 SEQ ID 5 MVC E GKRSASCP CFFLLTAKFYWIL

SEQ ID 1 AQKKGDIILGGLFPIHFGVAAKDQD
 SEQ ID 2 TSEGCQIIHPPWEGGIRYRGLTRDQ
 SEQ ID 3 PVWASHSPHLPRPHSRVPPHPSSER
 SEQ ID 4 LLLLPLLLPLAPGAWGWARGAPRPP
 SEQ ID 5 TMMQRTHSQEYAH SIRVDGDIILGG

SEQ ID 1 LKSRPESVECI RYNFRGFRWLQAMI
 SEQ ID 2 VKA INFLPVDYEIEYVCRGEREVVG
 SEQ ID 3 RAVYIGALFPMSSGGWPGGQACQPAV
 SEQ ID 4 PSSPPLSIMGLMPLTKEVAKGSI GR
 SEQ ID 5 LFPVHAKGERGVPCGELKKEKGIHR

SEQ ID 1 FAIEEINSSPALLPNLT LGYRIFD T
 SEQ ID 2 PKVRKCLANGSWTDM DTPSRCVRIC
 SEQ ID 3 EMAL EDVNSRRDILPDYELKLIHHD
 SEQ ID 4 GVLPAVELAIEQIRNESLLRPYFLD
 SEQ ID 5 LEAMLYAIDQINKDPDLLSNITLG V

SEQ ID 1 CNTVSKALEATLSFVAQNKIDSLNL
 SEQ ID 2 SKSYLTLENGKVFLTGGDLPALDGA
 SEQ ID 3 SKCDPGQATKYLYELLYNDPIKII L
 SEQ ID 4 LRLYDTECDNAKGLKAFYDAIKYGP
 SEQ ID 5 RILDTC SRD TYALEQSLTFVQALIE

SEQ ID 1 DEF C NCSEHIPSTIAVVGATGSGVS
 SEQ ID 2 RVD FRCDPDFHLVGSSRSICSQGQW
 SEQ ID 3 MPGCSSVSTLVAEAARMWN LIVLSY
 SEQ ID 4 NHLMVFGGVCPSVTSIIAESLQGWN
 SEQ ID 5 K D A S D V K C A N G D P P I F T K P D K I S G V

SEQ ID 1 TAVANLLGLFYIPQVSYASSSRLLS
 SEQ ID 2 STPKPHCQVNRTPHSERRAVYIGAL
 SEQ ID 3 GSSSPALSNRQRFPTFFRTHPSATL
 SEQ ID 4 LVQLSFAATT PVLADKKKYPYFFRT
 SEQ ID 5 IGA A A S S V S I M V A N I L R L F K I P Q I S

Figure 1a

SEQ ID 1 NKNQFKSFLRTIPNDEHQATAMADI
 SEQ ID 2 FPMSSGGWPGGQACQPAVEMALEDVN
 SEQ ID 3 HNPTRVKLFEKWGWKKIATIQQTTE
 SEQ ID 4 VPSDNAVNPAIILKLLKHYYQWKRVGT
 SEQ ID 5 YASTAPELSDNTRYDFFSRVVPDSS

SEQ ID 1 IEYFRWNWVGTTIAADDDYGRPGIEK
 SEQ ID 2 SRRDILPDYELKLIHHDSKCDPGQA
 SEQ ID 3 VFTSTLDDLEERVKEAGIEITFRQS
 SEQ ID 4 LTQDVQRFSEVRNDLTGVLYGEDIE
 SEQ ID 5 YQAQAMVDIVTALGWNYVSTLASEG

SEQ ID 1 FREEABERDICI DFSELISQYSDEE
 SEQ ID 2 TKYLYELLYNDDPIKII LMPGCSSVS
 SEQ ID 3 FFSDPAVPVKNLKRQDARIIVGLFY
 SEQ ID 4 ISDTESFSNDPCTSVKKLKGNDVRI
 SEQ ID 5 NYGESGV EAF TQISREIGGVCI AQS

SEQ ID 1 EIQHVVEVIQNSTAKVIVVFSSGPD
 SEQ ID 2 TLVABAAARMWNLI VLSYSSSSPALS
 SEQ ID 3 ETEARKVFCEVYKERLFGKKYVWFL
 SEQ ID 4 ILGQFDQNMAAKVFCCAYEENMYGS
 SEQ ID 5 QKIPREPRPGEF EKIIKRLLLETPNA

SEQ ID 1 LEPLIKEIVRRNITGKIWLASEAWA
 SEQ ID 2 NRQRFPTFFRTHPSATLHNPTRVKL
 SEQ ID 3 IGWYADNWFKIYDPSINCTVDEMTE
 SEQ ID 4 KYQWII PGWYEP S WVEQVHTEANSS
 SEQ ID 5 RAVIMFANEDDIRRI LEAAKKLNQS

SEQ ID 1 SSSLIAMPQYFHVVG GTIGFALKAG
 SEQ ID 2 FEKWGWKKIATIQQTTEVFTSTLDD
 SEQ ID 3 AVEGHITTEIVMLNPANTRSSISNMT
 SEQ ID 4 RCLRKNNLLAAMEGYIGVDFEPLSSK
 SEQ ID 5 GHFLWIGSDSWGSKIAPVYQQEEIA

SEQ ID 1 QIPGFR EFLKKVHPRKSVHNGFAKE
 SEQ ID 2 LEERVKEAGIEITFRQSF FSDPAVP
 SEQ ID 3 SQEFVEKLT KRLKRHP EETGGFQEA
 SEQ ID 4 QIKTISGKTPQQYEREYNNKRSGVG
 SEQ ID 5 EGAVTILPKRASIDGFDRYFRSRTL

Figure 1b

SEQ ID 1 F W E E T F N C H L Q E G A K G P L P V D T F L R
 SEQ ID 2 V K N L K R Q D A R I I V G L F Y E T E A R K V F
 SEQ ID 3 P L A Y D A I W A L A L A L N K T S G G G G R S G
 SEQ ID 4 P S K F H G Y A Y D G I W V I A K T L Q R A M E T
 SEQ ID 5 A N N R R N V W F A E F W E E N F G C K L G S H G

SEQ ID 1 G H E E S G D R F S N S S T A F R P L C T G D E N
 SEQ ID 2 C E V Y K E R L F G K K Y V W F L I G W Y A D N W
 SEQ ID 3 V R L E D F N Y N N Q T I T D Q I Y R A M N S S S
 SEQ ID 4 L H A S S R H Q R I Q D F N Y T D H T L G R I I L
 SEQ ID 5 K R N S H I K K C T G L E R I A R D S S Y E Q E G

SEQ ID 1 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y
 SEQ ID 2 F K I Y D P S I N C T V D E M T E A V E G H I T T
 SEQ ID 3 F E G V S G H V V F D A S G S R M A W T L I E Q L
 SEQ ID 4 N A M N E T N F F G V T G Q V V F R N G E R M G T
 SEQ ID 5 K V Q F V I D A V Y S M A Y A L H N M H K D L C P

SEQ ID 1 S I A H A L Q D I Y T C L P G R G L F T N G S C A
 SEQ ID 2 E I V M L N P A N T R S I S N M T S Q E F V E K L
 SEQ ID 3 Q G G S Y K K I G Y Y D S T K D D L S W S K T D K
 SEQ ID 4 I K F T Q F Q D S R E V K V G E Y N A V A D T L E
 SEQ ID 5 G Y I G L C P R M S T I D G K E L L G Y I R A V N

SEQ ID 1 D I K K V E A W Q V L K H L R H L N F T N N M G B
 SEQ ID 2 T K R L K R H P E E T G G F Q E A P L A Y D A I W
 SEQ ID 3 W I G G S P P A D Q T L V I K T F R F L S Q K
 SEQ ID 4 I I N D T I R F Q G S E P P K D K T I I L E Q L R
 SEQ ID 5 F N G S A G T P V T F N E N G D A P G R Y D I F Q

SEQ ID 1 Q V T F D E C G D L V G N Y S I I N W H L S P E D
 SEQ ID 2 A L A L A L N K T S G G G G R S G V R L E D F N Y
 SEQ ID 3
 SEQ ID 4 K I S L P
 SEQ ID 5 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E

SEQ ID 1 G S I V F K E V G Y Y N V Y A K K G E R L F I N E
 SEQ ID 2 N N Q T I T D Q I Y R A M N S S S F E G V S G H V
 SEQ ID 3
 SEQ ID 4
 SEQ ID 5 D M Q W A H R E H T H P A S V C S L P C K P G E R

Figure 1c

SEQ ID 1 E K I L W S G F S R E V P F S N C S R D C L A G T
SEQ ID 2 V F D A S G S R M A W T L I E Q L Q G G S Y K K I
SEQ ID 3
SEQ ID 4
SEQ ID 5 K K T V K G V P C C W H C E R C E G Y N Y Q V D E

SEQ ID 1 R K G I I E G E P T C C F E C V E C P D G E Y S D
SEQ ID 2 G Y Y D S T K D D L S W S K T D K W I G G S P P A
SEQ ID 3
SEQ ID 4
SEQ ID 5 L S C E L C P L D Q R P N M N R T G C Q L I P I I

SEQ ID 1 E T D A S A C N K C P D D F W S N E N H T S C I A
SEQ ID 2 D Q T L V I K T F R F L S Q K
SEQ ID 3
SEQ ID 4
SEQ ID 5 K L E W H S P W

SEQ ID 1 K E I E F L S W T E P F
SEQ ID 2
SEQ ID 3
SEQ ID 4
SEQ ID 5

Figure 1d

FIGURE 2a

SEQ ID 6 G I A L T L F A V L G I F L T A F V L G V F I K F R N T P I
SEQ ID 7 L F I S V S V L S S L G I V L A V V C L S F N I Y N S H V R
SEQ ID 8 L F I S V S V L S S L G I V L A V V C L S F N I Y N S H V R
SEQ ID 9 L Y S I L S A L T I L G M I M A S A F L F F N I K N R N Q K
SEQ ID 10 A V V P V F V A I L G I I A T T F V I V T F V R Y N D T P I

SEQ ID 6 V K A T N R E L S Y L L L F S L L C C F S S S L F F I G E P
SEQ ID 7 Y I Q N S Q P N L N N L T A V G C S L A L A A V F P L G L D
SEQ ID 8 Y I Q N S Q P N L N N L T A V G C S L A L A A V F P L G L D
SEQ ID 9 L I K M S S P Y M N N L I I L G G M L S Y A S I F L F G L D
SEQ ID 10 V R A S G R E L S Y V L L T G I F L C Y S I T F L M I A A P

SEQ ID 6 Q D W T C R L R Q P A F G I S F V L C I S C I L V K T N R V
SEQ ID 7 G Y H I G R N Q F P F V C Q A R L W L L G L G F S L G Y G S
SEQ ID 8 G Y H I G R N Q F P F V C Q A R L W L L G L G F S L G Y G S
SEQ ID 9 G S F V S E K T F E T L C T V R T W I L T V G Y T T A F G A
SEQ ID 10 D T I I C S F R R V F L G L G M C F S Y A A L L T K T N R I

SEQ ID 6 L L V F E A K I P T S F H R K W W G L N L Q F L L V F L C T
SEQ ID 7 M F T K I W W V H T V F T K K E E K K E W R K T L E P W K L
SEQ ID 8 M F T K I W W V H T V F T K K E E K K E W R K T L E P W K L
SEQ ID 9 M F A K T W R V H A I F K N V K M K K K I I K D Q K L L V I
SEQ ID 10 H R I F E Q G K K S V T A P K F I S P A S Q L V I T F S L I

SEQ ID 6 F M Q I V I C V I W L Y T A P P S S Y R N Q E L E D E I I F
SEQ ID 7 Y A T V G L L V G M D V L T L A I W Q I V D P L H R T I E T
SEQ ID 8 Y A T V G L L V G M D V L T L A I W Q I V D P L H R T I E T
SEQ ID 9 V G G M L L I D L C I L I C W Q A V D P L R R T V E K Y S M
SEQ ID 10 S V Q L L G V F V W F V V D P P H I I I D Y G E Q R T L D P

SEQ ID 6 I T C H E G S L M A L G F L I G Y T C L L A A I C F F F A F
SEQ ID 7 F A K E E P K E D I D V S I L P Q L E H C S S R K M N T W L
SEQ ID 8 F A K E E P K E D I D V S I L P Q L E H C S S R K M N T W L
SEQ ID 9 E P D P A G R D I S I R P L L E H C E N T H M T I W L G I V
SEQ ID 10 E K A R G V L K C D I S D L S L I C S L G Y S I L L M V T C

SEQ ID 6 K S R K L P E N F N E A K F I T F S M L I F F I V W I S F I
SEQ ID 7 G I F Y G Y K G L L L L L G I F L A Y E T K S V S T E K I N
SEQ ID 8 G I F Y G Y K G L L L L L G I F L A Y E T K S V S T E K I N
SEQ ID 9 Y A Y K G L L M L F G C F L A W E T R N V S I P A L N D S K
SEQ ID 10 T V Y A I K T R G V P E T F N E A K P I G F T M Y T T C I I

FIGURE 3a

SEQ ID 11 K P S R N T I E E V R C S T A A H A F K V A A R A T L R R S
SEQ ID 12 R R L I T R G E W Q S E A Q D T M K T G S S T N N N E E E K
SEQ ID 13 R R L I T R G E W Q S E A Q D T M K T G S S T N N N E E E K
SEQ ID 14 I T L R T N P D A A T Q N R R F Q F T Q N Q K K E D S K T S
SEQ ID 15 H P E Q N V Q K R K R S F K A V V T A A T M Q S K L I Q K G

SEQ ID 11 N V S R K R S S S L G G S T G S T P S S S I S S K S N S E D
SEQ ID 12 S R L L E K E N R E L E K I I A E K E E R V S E L R H Q L Q
SEQ ID 13 S R L L E K E N R E L E K I I A E K E E R V S E L R H Q L Q
SEQ ID 14 T S V T S V N Q A S T S R L E G L Q S E N H R L R M K I T E
SEQ ID 15 N D R P N G E V K S E L C E S L E T N S K S S V E F P M V K

SEQ ID 11 P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L T L P Q
SEQ ID 12 S R Q Q L R S R R H P P T P P E P S G G L P R G P P E P P D
SEQ ID 13 S R Q Q L R S R R H P P T P P E P S G G L P R G P P E P P D
SEQ ID 14 L D K D L E E V T M Q L Q D T P E K T T Y I K Q N H Y Q E L
SEQ ID 15 S G S T S

SEQ ID 11 Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S F D E P
SEQ ID 12 R L S C D G S R V H L L Y K
SEQ ID 13 R L S C D G S R V H L L Y K
SEQ ID 14 N D I L N L G N F T E S T D G G K A I L K N H L D Q N P Q L
SEQ ID 15

SEQ ID 11 Q K N A M A H G N S T H Q N S L E A Q K S S D T L T R H Q P
SEQ ID 12
SEQ ID 13
SEQ ID 14 Q W N T T E P S R T C K D P I E D I N S P E H I Q R R L S L
SEQ ID 15

SEQ ID 11 L L P L Q C G E T D L D L T V Q E T G L Q G P V G G D Q R P
SEQ ID 12
SEQ ID 13
SEQ ID 14 Q L P I L H H A Y L P S I G G V D A S C V S P C V S P T A S
SEQ ID 15

SEQ ID 11 E V E D P E E L S P A L V V S S S Q S F V I S G G G S T V T
SEQ ID 12
SEQ ID 13
SEQ ID 14 P R H R H V P P S F R V M V S G L
SEQ ID 15

[illegible]

SEQ ID 12

SEQ ID 13

SEQ ID 14

SEQ ID 15

[illegible]

FIGURE 4a

SEQ. ID. NO. 16 M A R S L T W G C C P W C L T E E E K T A A R I D Q E I N R
SEQ. ID. NO. 17 M A R S L T W R C C P W C L T E D E K A A A R V D Q E I N R

SEQ. ID. NO. 16 I L L E Q K K Q E R E E L K L L L L G P G E S G K S T F I K
SEQ. ID. NO. 17 I L L E Q K K Q D R G E L K L L L L G P G E S G K S T F I K

SEQ. ID. NO. 16 Q M R I I H G V G Y S E E D R R A F R L L I Y Q N I F V S M
SEQ. ID. NO. 17 Q M R I I H G A G Y S E E E R K G F R P L V Y Q N I F V S M

SEQ. ID. NO. 16 Q A M I D A M D R L Q I P F S R P D S K Q H A S L V M T Q D
SEQ. ID. NO. 17 R A M I E A M E R L Q I P F S R P E S K H H A S L V M S Q D

SEQ. ID. NO. 16 P Y K V S T F E K P Y A V A M Q Y L W R D A G I R A C Y E R
SEQ. ID. NO. 17 P Y K V T T F E K R Y A A A M Q W L W R D A G I R A C Y E R

SEQ. ID. NO. 16 R R E F H L L D S A V Y Y L S H L E R I S E D S Y I P T A Q
SEQ. ID. NO. 17 R R E F H L L D S A V Y Y L S H L E R I T E E G Y V P T A Q

SEQ. ID. NO. 16 D V L R S R M P T T G I N E Y C F S V K K T K L R I V D V G
SEQ. ID. NO. 17 D V L R S R M P T T G I N E Y C F S V Q K T N L R I V D V G

SEQ. ID. NO. 16 G Q R S E R R K W I H C F E N V I A L I Y L A S L S E Y D Q
SEQ. ID. NO. 17 G Q K S E R K K W I H C F E N V I A L I Y L A S L S E Y D Q

SEQ. ID. NO. 16 C L E E N D Q E N R M E E S L A L F S T I L E L P W F K S T
SEQ. ID. NO. 17 C L E E N N Q E N R M K E S L A L F G T I L E L P W F K S T

SEQ. ID. NO. 16 S V I L F L N K T D I L E D K I H T S H L A T Y F P S F Q G
SEQ. ID. NO. 17 S V I L F L N K T D I L E E K I P T S H L A T Y F P S F Q G

SEQ. ID. NO. 16 P R R D A E A A K S F I L D M Y A R V Y A S C A E P Q D G G
SEQ. ID. NO. 17 P K Q D A E A A K R F I L D M Y T R M Y T G C V D G P E G S

SEQ. ID. NO. 16 R K G S R A R R F F A H F T C A T D T Q S V R S V F K D V R
SEQ. ID. NO. 17 K K G A R S R R L F S H Y T C A T D T Q N I R K V F K D V R

FIGURE 4b

SEQ. ID. NO. 16 D S V L A R Y L D E I N L L
SEQ. ID. NO. 17 D S V L A R Y L D E I N L L

ClustalW Formatted Alignments

SEQ. ID. NO. 18 A T G G C A T T T T A T A G C T G C T G C T G G G
 SEQ. ID. NO. 19 A T G T T G C T G C T G C T A C T G G C G C
 SEQ. ID. NO. 20 A T G G G G C C C G G G G C C C T T T T G C C C
 SEQ. ID. NO. 21 A T G G C T T C C C C G C G G A G C T C C G G G C

SEQ. ID. NO. 18 T C C T C T T G G C A C T C A C C T G G C A C A C
 SEQ. ID. NO. 19 C A C T C T T C C T C C G C C C C C G G G C G C
 SEQ. ID. NO. 20 G G G T G G G G T G G C C A C T G C C G C T T C T
 SEQ. ID. NO. 21 A G C C C G G G C C G C - G C C G C C G C C G C C

SEQ. ID. NO. 18 C T C T G C C T A C G G G C C A G A C C A G C G A
 SEQ. ID. NO. 19 G G G C G G G G C G C A G A C C C C C A A C G C C
 SEQ. ID. NO. 20 G G T T G T G A T G G C G G C A G G G G T G G C T
 SEQ. ID. NO. 21 A C C G C C G C C C G C G C G C C T G C T A C T G

SEQ. ID. NO. 18 G C C C A A A A G A A G G G G G A C A T T A T C C
 SEQ. ID. NO. 19 A C C T C A G A A G G T T G C C A G A T C A T A C
 SEQ. ID. NO. 20 C C G G T G T G G G C C T C C C A C T C C C C C C
 SEQ. ID. NO. 21 C T A C T G C T G C T G C C G C T G C T G C T G C

SEQ. ID. NO. 18 T T G G G G G G C T C T T T C C T A T T C A T T T
 SEQ. ID. NO. 19 A C C C G C C C T G G G A A G G G G G C A T C A G
 SEQ. ID. NO. 20 A T C T C C C G C G G C C T C A C T C G C G G G T
 SEQ. ID. NO. 21 C T C T G G C G C C C G G G G C C T G G G G C T G

SEQ. ID. NO. 18 T G G A G T A G C A G C T A A A G A T C A A G A T
 SEQ. ID. NO. 19 G T A C C G G G G C C T G A C T C G G G A C C A G
 SEQ. ID. NO. 20 C C C C C G C A C C C C T C C T C A G A A C G G
 SEQ. ID. NO. 21 G G C G C G G G G C G C C C C C C G G C C G C C G

SEQ. ID. NO. 18 C T C A A A T C A A G G C C G G A G T C T G T G G
 SEQ. ID. NO. 19 G T G A A G G C T A T C A A C T T C C T G C C A G
 SEQ. ID. NO. 20 C G C G C A G T G T A C A T C G G G G C A C T G T
 SEQ. ID. NO. 21 C C C A G C A G C C C G C C G C T C T C C A T C A

SEQ. ID. NO. 18 A A T G T A T C A G G T A T A A T T T C C G T G G
 SEQ. ID. NO. 19 T G G A C T A T G A G A T T G A G T A T G T G T G
 SEQ. ID. NO. 20 T T C C C A T G A G C G G G G G C T G G C C A G G
 SEQ. ID. NO. 21 T G G G C C T C A T G C C G C T C A C C A A G G A

Figure 5a

SEQ. ID. NO. 18 G T T T C G C T G G T T A C A G G C T A T G A T A
 SEQ. ID. NO. 19 C C G G G G G G A G C G C G A G G T G G T G G G G
 SEQ. ID. NO. 20 G G G C C A G G C C T G C C A G C C C G C G G T G
 SEQ. ID. NO. 21 G G T G G C C A A G G G C A G C A T C G G G C G C

SEQ. ID. NO. 18 T T T G C C A T A G A G G A G A T A A A C A G C A
 SEQ. ID. NO. 19 C C C A A G G T C C G C A A G T G C C T G G C C A
 SEQ. ID. NO. 20 G A G A T G G C G C T G G A G G A C G T G A A T A
 SEQ. ID. NO. 21 G G T G T G C T C C C C G C C G T G G A A C T G G

SEQ. ID. NO. 18 G C C C A G C C C T T C T T C C C A A C T T G A C
 SEQ. ID. NO. 19 A C G G C T C C T G G A C A G A T A T G G A C A C
 SEQ. ID. NO. 20 G C C G C A G G G A C A T C C T G C C G G A C T A
 SEQ. ID. NO. 21 C C A T C G A G C A G A T C C G C A A C G A G T C

SEQ. ID. NO. 18 G C T G G G A T A C A G G A T A T T T G A C A C T
 SEQ. ID. NO. 19 A C C C A G C C G C T G T G T C C G A A T C T G C
 SEQ. ID. NO. 20 T G A G C T C A A G C T C A T C C A C C A C G A C
 SEQ. ID. NO. 21 A C T C C T G C G C C C C T A C T T C C T C G A C

SEQ. ID. NO. 18 T G C A A C A C C G T T T C T A A G G C C T T G G
 SEQ. ID. NO. 19 T C C A A G T C T T A T T T G A C C C T G G A A A
 SEQ. ID. NO. 20 A G C A A G T G T G A T C C A G G C C A A G C C A
 SEQ. ID. NO. 21 C T G C G G C T C T A T G A C A C G G A G T G C G

SEQ. ID. NO. 18 A A G C C A C C C T G A G T T T T G T T G C T C A
 SEQ. ID. NO. 19 A T G G G A A G G T T T T C C T G A C G G G T G G
 SEQ. ID. NO. 20 C C A A G T A C C T A T A T G A G C T G C T C T A
 SEQ. ID. NO. 21 A C A A C G C A A A A G G G T T G A A A G C C T T

SEQ. ID. NO. 18 A A A C A A A A T T G A T T C T T T G A A C C T T
 SEQ. ID. NO. 19 G G A C C T C C C A G C T C T G G A C G G A G C C
 SEQ. ID. NO. 20 C A A C G A C C C T A T C A A G A T C A T C C T T
 SEQ. ID. NO. 21 C T A C G A T G C A A T A A A A T A C G G G C C G

SEQ. ID. NO. 18 G A T G A G T T C T G C A A C T G C T C A G A G C
 SEQ. ID. NO. 19 C G G G T G G A T T T C C G G T G T G A C C C C G
 SEQ. ID. NO. 20 A T G C C T G G C T G C A G C T C T G T C T C C A
 SEQ. ID. NO. 21 A A C C A C T T G A T G G T G T T T G G A G G C G

Figure 5b

SEQ. ID. NO. 18 A C A T T C C C T C T A C G A T T G C T G T G G T
 SEQ. ID. NO. 19 A C T T C C A T C T G G T G G G C A G C T C C C G
 SEQ. ID. NO. 20 C G C T G G T G G C T G A G G C T G C T A G G A T
 SEQ. ID. NO. 21 T C T G T C C A T C C G T C A C A T C C A T C A T

SEQ. ID. NO. 18 G G G A G C A A C T G G C T C A G G C G T C T C C
 SEQ. ID. NO. 19 G A G C A T C T G T A G T C A G G G C C A G T G G
 SEQ. ID. NO. 20 G T G G A A C C T C A T T G T G C T T T C C T A T
 SEQ. ID. NO. 21 T G C A G A G T C C C T C C A A G G C T G G A A T

SEQ. ID. NO. 18 A C G G C A G T G G C A A A T C T G C T G G G G C
 SEQ. ID. NO. 19 A G C A C C C C C A A G C C C C A C T G C C A G G
 SEQ. ID. NO. 20 G G C T C C A G C T C A C C A G C C C T G T C A A
 SEQ. ID. NO. 21 C T G G T G C A G C T T T C T T T T G C T G C A A

SEQ. ID. NO. 18 T C T T C T A C A T T C C C C A G G T C A G T T A
 SEQ. ID. NO. 19 T G A A T C G A A C G C C A C A C T C A G A A C G
 SEQ. ID. NO. 20 A C C G G C A G C G T T T C C C C A C T T T C T T
 SEQ. ID. NO. 21 C C A C G C C T G T T C T A G C C G A T A A G A A

SEQ. ID. NO. 18 T G C C T C C T C C A G C A G A C T C C T C A G C
 SEQ. ID. NO. 19 G C G C G C A G T G T A C A T C G G G G C A C T G
 SEQ. ID. NO. 20 C C G A A C G C A C C C A T C A G C C A C A C T C
 SEQ. ID. NO. 21 A A A A T A C C C T T A T T T C T T T C G G A C C

SEQ. ID. NO. 18 A A C A A G A A T C A A T T C A A G T C T T T C C
 SEQ. ID. NO. 19 T T T C C C A T G A G C G G G G G C T G G C C A G
 SEQ. ID. NO. 20 C A C A A C C C T A C C C G C G T G A A A C T C T
 SEQ. ID. NO. 21 G T C C C A T C A G A C A A T G C G G T G A A T C

SEQ. ID. NO. 18 T C C G A A C C A T C C C C A A T G A T G A G C A
 SEQ. ID. NO. 19 G G G G C C A G G C C T G C C A G C C C G C G G T
 SEQ. ID. NO. 20 T T G A A A A G T G G G G C T G G A A G A A G A T
 SEQ. ID. NO. 21 C A G C C A T T C T G A A G T T G C T C A A G C A

SEQ. ID. NO. 18 C C A G G C C A C T G C C A T G G C A G A C A T C
 SEQ. ID. NO. 19 G G A G A T G G C G C T G G A G G A C G T G A A T
 SEQ. ID. NO. 20 T G C T A C C A T C C A G C A G A C C A C T G A G
 SEQ. ID. NO. 21 C T A C C A G T G G A A G C G C G T G G G C A C G

Figure 5c

SEQ. ID. NO. 18 A T C G A G T A T T T C C G C T G G A A C T G G G
 SEQ. ID. NO. 19 A G C C G C A G G G A C A T C C T G C C G G A C T
 SEQ. ID. NO. 20 G T C T T C A C T T C G A C T C T G G A C G A C C
 SEQ. ID. NO. 21 C T G A C G C A A G A C G T T C A G A G G T T C T

SEQ. ID. NO. 18 T G G G C A C A A T T G C A G C T G A T G A C G A
 SEQ. ID. NO. 19 A T G A G C T C A A G C T C A T C C A C C A C G A
 SEQ. ID. NO. 20 T G G A G G A A C G A G T G A A G G A G G C T G G
 SEQ. ID. NO. 21 C T G A G G T G C G G A A T G A C C T G A C T G G

SEQ. ID. NO. 18 C T A T G G G C G G C C G G G G A T T G A G A A A
 SEQ. ID. NO. 19 C A G C A A G T G T G A T C C A G G C C A A G C C
 SEQ. ID. NO. 20 A A T T G A G A T T A C T T T C C G C C A G A G T
 SEQ. ID. NO. 21 A G T T C T G T A T G G C G A G G A C A T T G A G

SEQ. ID. NO. 18 T T C C G A G A G G A A G C T G A G G A A A G G G
 SEQ. ID. NO. 19 A C C A A G T A C C T A T A T G A G C T G C T C T
 SEQ. ID. NO. 20 T T C T T C T C A G A T C C A G C T G T G C C C G
 SEQ. ID. NO. 21 A T T T C A G A C A C C G A G A G C T T C T C C A

SEQ. ID. NO. 18 A T A T C T G C A T C G A C T T C A G T G A A C T
 SEQ. ID. NO. 19 A C A A C G A C C C T A T C A A G A T C A T C C T
 SEQ. ID. NO. 20 T C A A A A A C C T G A A G C G C C A G G A T G C
 SEQ. ID. NO. 21 A C G A T C C C T G T A C C A G T G T C A A A A A

SEQ. ID. NO. 18 C A T C T C C C A G T A C T C T G A T G A G G A A
 SEQ. ID. NO. 19 T A T G C C T G G C T G C A G C T C T G T C T C C
 SEQ. ID. NO. 20 C C G A A T C A T C G T G G G A C T T T T C T A T
 SEQ. ID. NO. 21 G C T G A A G G G G A A T G A T G T G C G G A T C

SEQ. ID. NO. 18 G A G A T C C A G C A T G T G G T A G A G G T G A
 SEQ. ID. NO. 19 A C G C T G G T G G C T G A G G C T G C T A G G A
 SEQ. ID. NO. 20 G A G A C T G A A G C C C G G A A A G T T T T T
 SEQ. ID. NO. 21 A T C C T T G G C C A G T T T G A C C A G A A T A

SEQ. ID. NO. 18 T T C A A A A T T C C A C G G C C A A A G T C A T
 SEQ. ID. NO. 19 T G T G G A A C C T C A T T G T G C T T T C C T A
 SEQ. ID. NO. 20 G T G A G G T G T A C A A G G A G C G T C T C T T
 SEQ. ID. NO. 21 T G G C A G C A A A A G T G T T C T G T T G T G C

Figure 5d

SEQ. ID. NO. 18 C G T G G T T T T C T C C A G T G G C C C A G A T
 SEQ. ID. NO. 19 T G G C T C C A G C T C A C C A G C C C T G T C A
 SEQ. ID. NO. 20 T G G G A A G A A G T A C G T C T G G T T C C T C
 SEQ. ID. NO. 21 A T A C G A G G A G A A C A T G T A T G G T A G T

SEQ. ID. NO. 18 C T T G A G C C C C T C A T C A A G G A G A T T G
 SEQ. ID. NO. 19 A A C C G G C A G C G T T T C C C C A C T T T C T
 SEQ. ID. NO. 20 A T T G G G T G G T A T G C T G A C A A T T G G T
 SEQ. ID. NO. 21 A A A T A T C A G T G G A T C A T T C C G G G C T

SEQ. ID. NO. 18 T C C G G C G C A A T A T C A C G G G C A A G A T
 SEQ. ID. NO. 19 T C C G A A C G C A C C C A T C A G C C A C A C T
 SEQ. ID. NO. 20 T C A A G A T C T A C G A C C C T T C T A T C A A
 SEQ. ID. NO. 21 G G T A C G A G C C T T C T T G G T G G G A G C A

SEQ. ID. NO. 18 C T G G C T G G C C A G C G A G G C C T G G G C C
 SEQ. ID. NO. 19 C C A C A A C C C T A C C C G C G T G A A A C T C
 SEQ. ID. NO. 20 C T G C A C A G T G G A T G A G A T G A C T G A G
 SEQ. ID. NO. 21 G G T G C A C A C G G A A G C C A A C T C A T C C

SEQ. ID. NO. 18 A G C T C C T C C C T G A T C G C C A T G C C T C
 SEQ. ID. NO. 19 T T T G A A A A G T G G G G C T G G A A G A A G A
 SEQ. ID. NO. 20 G C G G T G G A G G G C C A C A T C A C A A C T G
 SEQ. ID. NO. 21 C G C T G C C T C C G G A A G A A T C T G C T T G

SEQ. ID. NO. 18 A G T A C T T C C A C G T G G T T G G C G G C A C
 SEQ. ID. NO. 19 T T G C T A C C A T C C A G C A G A C C A C T G A
 SEQ. ID. NO. 20 A G A T T G T C A T G C T G A A T C C T G C C A A
 SEQ. ID. NO. 21 C T G C C A T G G A G G G C T A C A T T G G C G T

SEQ. ID. NO. 18 C A T T G G A T T C G C T C T G A A G G C T G G G
 SEQ. ID. NO. 19 G G T C T T C A C T T C G A C T C T G G A C G A C
 SEQ. ID. NO. 20 T A C C C G C A G C A T T T C C A A C A T G A C A
 SEQ. ID. NO. 21 G G A T T T C G A G C C C C T G A G C T C C A A G

SEQ. ID. NO. 18 C A G A T C C C A G G C T T C C G G G A A T T C C
 SEQ. ID. NO. 19 C T G G A G G A A C G A G T G A A G G A G G C T G
 SEQ. ID. NO. 20 T C C C A G G A A T T T G T G G A G A A A C T A A
 SEQ. ID. NO. 21 C A G A T C A A G A C C A T C T C A G G A A A G A

Figure 5e

SEQ. ID. NO. 18 T G A A G A A G G T C C A T C C C A G G A A G T C
 SEQ. ID. NO. 19 G A A T T G A G A T T A C T T T C C G C C A G A G
 SEQ. ID. NO. 20 C C A A G C G A C T G A A A A G A C A C C C T G A
 SEQ. ID. NO. 21 C T C C A C A G C A G T A T G A G A G A G A G T A

SEQ. ID. NO. 18 T G T C C A C A A T G G T T T T G C C A A G G A G
 SEQ. ID. NO. 19 T T T C T T C T C A G A T C C A G C T G T G C C C
 SEQ. ID. NO. 20 G G A G A C A G G A G G C T T C C A G G A G G C A
 SEQ. ID. NO. 21 C A A C A A C A A G C G G T C A G G C G T G G G G

SEQ. ID. NO. 18 T T T T G G G A A G A A A C A T T T A A C T G C C
 SEQ. ID. NO. 19 G T C A A A A A C C T G A A G C G C C A G G A T G
 SEQ. ID. NO. 20 C C G C T G G C C T A T G A T G C C A T C T G G G
 SEQ. ID. NO. 21 C C C A G C A A G T T C C A C G G G T A C G C C T

SEQ. ID. NO. 18 A C C T C C A A G A A G G T G C A A A A G G A C C
 SEQ. ID. NO. 19 C C C G A A T C A T C G T G G G A C T T T T C T A
 SEQ. ID. NO. 20 C C T T G G C A C T G G C C C T G A A C A A G A C
 SEQ. ID. NO. 21 A C G A T G G C A T C T G G G T C A T C G C C A A

SEQ. ID. NO. 18 T T T A C C T G T G G A C A C C T T T C T G A G A
 SEQ. ID. NO. 19 T G A G A C T G A A G C C C G G A A A G T T T T T
 SEQ. ID. NO. 20 A T C T G G A G G A G G C G G C C G T T C T G G T
 SEQ. ID. NO. 21 G A C A C T G C A G A G G G C C A T G G A G A C A

SEQ. ID. NO. 18 G G T C A C G A A G A A A G T G G C G A C A G G T
 SEQ. ID. NO. 19 T G T G A G G T G T A C A A G G A G C G T C T C T
 SEQ. ID. NO. 20 G T G C G C C T G G A G G A C T T C A A C T A C A
 SEQ. ID. NO. 21 C T G C A T G C C A G C A G C C G G C A C C A G C

SEQ. ID. NO. 18 T T A G C A A C A G C T C G A C A G C C T T C C G
 SEQ. ID. NO. 19 T T G G G A A G A A G T A C G T C T G G T T C C T
 SEQ. ID. NO. 20 A C A A C C A G A C C A T T A C C G A C C A A A T
 SEQ. ID. NO. 21 G G A T C C A G G A C T T C A A C T A C A C G G A

SEQ. ID. NO. 18 A C C C C T C T G T A C A G G G G A T G A G A A C
 SEQ. ID. NO. 19 C A T T G G G T G G T A T G C T G A C A A T T G G
 SEQ. ID. NO. 20 C T A C C G G G C A A T G A A C T C T T C G T C C
 SEQ. ID. NO. 21 C C A C A C G C T G G G C A G G A T C A T C C T C

Figure 5f

SEQ. ID. NO. 18 A T C A G C A G T G T C G A G A C C C C T T A C A
 SEQ. ID. NO. 19 T T C A A G A T C T A C G A C C C T T C T A T C A
 SEQ. ID. NO. 20 T T T G A G G G T G T C T C T G G C C A T G T G G
 SEQ. ID. NO. 21 A A T G C C A T G A A C G A G A C C A A C T T C T

SEQ. ID. NO. 18 T A G A T T A C A C G C A T T T A C G G A T A T C
 SEQ. ID. NO. 19 A C T G C A C A G T G G A T G A G A T G A C T G A
 SEQ. ID. NO. 20 T G T T T G A T G C C A G C G G C T C T C G G A T
 SEQ. ID. NO. 21 T C G G G G T C A C G G G T C A A G T T G T A T T

SEQ. ID. NO. 18 C T A C A A T G T G T A C T T A G C A G T C T A C
 SEQ. ID. NO. 19 G G C G G T G G A G G G C C A C A T C A C A A C T
 SEQ. ID. NO. 20 G G C A T G G A C G C T T A T C G A G C A G C T T
 SEQ. ID. NO. 21 C C G G A A T G G G G A G A G A A T G G G G A C C

SEQ. ID. NO. 18 T C C A T T G C C C A C G C C T T G C A A G A T A
 SEQ. ID. NO. 19 G A G A T T G T C A T G C T G A A T C C T G C C A
 SEQ. ID. NO. 20 C A G G G T G G C A G C T A C A A G A A G A T T G
 SEQ. ID. NO. 21 A T T A A A T T T A C T C A A T T T C A A G A C A

SEQ. ID. NO. 18 T A T A T A C C T G C T T A C C T G G G A G A G G
 SEQ. ID. NO. 19 A T A C C C G C A G C A T T T T C C A A C A T G A C
 SEQ. ID. NO. 20 G C T A C T A T G A C A G C A C C A A G G A T G A
 SEQ. ID. NO. 21 G C A G G G A G G T G A A G G T G G G A G A G T A

SEQ. ID. NO. 18 G C T C T T C A C C A A T G G C T C C T G T G C A
 SEQ. ID. NO. 19 A T C C C A G G A A T T T G T G G A G A A A C T A
 SEQ. ID. NO. 20 T C T T T C C T G G T C C A A A A C A G A T A A A
 SEQ. ID. NO. 21 C A A C G C T G T G G C C G A C A C A C T G G A G

SEQ. ID. NO. 18 G A C A T C A A G A A A G T T G A G G C G T G G C
 SEQ. ID. NO. 19 A C C A A G C G A C T G A A A A G A C A C C C T G
 SEQ. ID. NO. 20 T G G A T T G G A G G G T C C C C C C C A G C T G
 SEQ. ID. NO. 21 A T C A T C A A T G A C A C C A T C A G G T T C C

SEQ. ID. NO. 18 A G G T C C T G A A G C A C C T A C G G C A T C T
 SEQ. ID. NO. 19 A G G A G A C A G G A G G C T T C C A G G A G G C
 SEQ. ID. NO. 20 A C C A G A C C C T G G T C A T C A A G A C A T T
 SEQ. ID. NO. 21 A A G G A T C C G A A C C A C C A A A A G A C A A

Figure 5g

SEQ. ID. NO. 18 A A A C T T T A C A A A C A A T A T G G G G G A G
 SEQ. ID. NO. 19 A C C G C T G G C C T A T G A T G C C A T C T G G
 SEQ. ID. NO. 20 C C G C T T C C T G T C A C A G A A A C T C T T T
 SEQ. ID. NO. 21 G A C C A T C A T C C T G G A G C A G C T G C G G

SEQ. ID. NO. 18 C A G G T G A C C T T T G A T G A G T G T G G T G
 SEQ. ID. NO. 19 G C C T T G G C A C T G G C C C T G A A C A A G A
 SEQ. ID. NO. 20 A T C T C C G T C T C A G T T C T C T C C A G C C
 SEQ. ID. NO. 21 A A G A T C T C C C T A C C T C T C T A C A G C A

SEQ. ID. NO. 18 A C C T G G T G G G G A A C T A T T C C A T C A T
 SEQ. ID. NO. 19 C A T C T G G A G G A G G C G G C C G T T C T G G
 SEQ. ID. NO. 20 T G G G C A T T G T C C T A G C T G T T G T C T G
 SEQ. ID. NO. 21 T C C T C T C T G C C C T C A C C A T C C T C G G

SEQ. ID. NO. 18 C A A C T G G C A C C T C T C C C C A G A G G A T
 SEQ. ID. NO. 19 T G T G C G C C T G G A G G A C T T C A A C T A C
 SEQ. ID. NO. 20 T C T G T C C T T T A A C A T C T A C A A C T C A
 SEQ. ID. NO. 21 G A T G A T C A T G G C C A G T G C T T T T C T C

SEQ. ID. NO. 18 G G C T C C A T C G T G T T T A A G G A A G T C G
 SEQ. ID. NO. 19 A A C A A C C A G A C C A T T A C C G A C C A A A
 SEQ. ID. NO. 20 C A T G T C C G T T A T A T C C A G A A C T C A C
 SEQ. ID. NO. 21 T T C T T C A A C A T C A A G A A C C G G A A T C

SEQ. ID. NO. 18 G G T A T T A C A A C G T C T A T G C C A A G A A
 SEQ. ID. NO. 19 T C T A C C G G G C A A T G A A C T C T T C G T C
 SEQ. ID. NO. 20 A G C C C A A C C T G A A C A A C C T G A C T G C
 SEQ. ID. NO. 21 A G A A G C T C A T A A A G A T G T C G A G T C C

SEQ. ID. NO. 18 G G G A G A A A G A C T C T T C A T C A A C G A G
 SEQ. ID. NO. 19 C T T T G A G G G T G T C T C T G G C C A T G T G
 SEQ. ID. NO. 20 T G T G G G C T G C T C A C T G G C T T T A G C T
 SEQ. ID. NO. 21 A T A C A T G A A C A A C C T T A T C A T C C T T

SEQ. ID. NO. 18 G A G A A A A T C C T G T G G A G T G G G T T C T
 SEQ. ID. NO. 19 G T G T T T G A T G C C A G C G G C T C T C G G A
 SEQ. ID. NO. 20 G C T G T C T T C C C C C T G G G G C T C G A T G
 SEQ. ID. NO. 21 G G A G G G A T G C T C T C C T A T G C T T C C A

Figure 5h

SEQ. ID. NO. 18 C C A G G G A G G T G C C C T T C T C C A A C T G
 SEQ. ID. NO. 19 T G G C A T G G A C G C T T A T C G A G C A G C T
 SEQ. ID. NO. 20 G T T A C C A C A T T G G G A G G A A C C A G T T
 SEQ. ID. NO. 21 T A T T T C T C T T T G G C C T T G A T G G A T C

SEQ. ID. NO. 18 C A G C C G A G A C T G C C T G G C A G G G A C C
 SEQ. ID. NO. 19 T C A G G G T G G C A G C T A C A A G A A G A T T
 SEQ. ID. NO. 20 T C C T T T C G T C T G C C A G G C C C G C C T C
 SEQ. ID. NO. 21 C T T T G T C T C T G A A A A G A C C T T T G A A

SEQ. ID. NO. 18 A G G A A A G G G A T C A T T G A G G G G G A G C
 SEQ. ID. NO. 19 G G C T A C T A T G A C A G C A C C A A G G A T G
 SEQ. ID. NO. 20 T G G C T C C T G G G C C T G G G C T T T A G T C
 SEQ. ID. NO. 21 A C A C T T T G C A C C G T C A G G A C C T G G A

SEQ. ID. NO. 18 C C A C C T G C T G C T T T G A G T G T G T G G A
 SEQ. ID. NO. 19 A T C T T T C C T G G T C C A A A A C A G A T A A
 SEQ. ID. NO. 20 T G G G C T A C G G T T C C A T G T T C A C C A A
 SEQ. ID. NO. 21 T T C T C A C C G T G G G C T A C A C G A C C G C

SEQ. ID. NO. 18 G T G T C C T G A T G G G G A G T A T A G T G A T
 SEQ. ID. NO. 19 A T G G A T T G G A G G G T C C C C C C C A G C T
 SEQ. ID. NO. 20 G A T T T G G T G G G T C C A C A C G G T C T T C
 SEQ. ID. NO. 21 T T T T G G G G C C A T G T T T G C A A A G A C C

SEQ. ID. NO. 18 G A G A C A G A T G C C A G T G C C T G T A A C A
 SEQ. ID. NO. 19 G A C C A G A C C C T G G T C A T C A A G A C A T
 SEQ. ID. NO. 20 A C A A A G A A G G A A G A A A A G A A G G A G T
 SEQ. ID. NO. 21 T G G A G A G T C C A C G C C A T C T T C A A A A

SEQ. ID. NO. 18 A G T G C C C A G A T G A C T T C T G G T C C A A
 SEQ. ID. NO. 19 T C C G C T T C C T G T C A C A G A A A C T C T T
 SEQ. ID. NO. 20 G G A G G A A G A C T C T G G A A C C C T G G A A
 SEQ. ID. NO. 21 A T G T G A A A A T G A A G A A G A A G A T C A T

SEQ. ID. NO. 18 T G A G A A C C A C A C C T C C T G C A T T G C C
 SEQ. ID. NO. 19 T A T C T C C G T C T C A G T T C T C T C C A G C
 SEQ. ID. NO. 20 G C T G T A T G C C A C A G T G G G C C T G C T G
 SEQ. ID. NO. 21 C A A G G A C C A G A A A C T G C T T G T G A T C

Figure 5i

SEQ. ID. NO. 18 A A G G A G A T C G A G T T T C T G T C G T G G A
 SEQ. ID. NO. 19 C T G G G C A T T G T C C T A G C T G T T G T C T
 SEQ. ID. NO. 20 G T G G G C A T G G A T G T C C T C A C T C T C G
 SEQ. ID. NO. 21 G T G G G G G G C A T G C T G C T G A T C G A C C

SEQ. ID. NO. 18 C G G A G C C C T T T G G G A T C G C A C T C A C
 SEQ. ID. NO. 19 G T C T G T C C T T T A A C A T C T A C A A C T C
 SEQ. ID. NO. 20 C C A T C T G G C A G A T C G T G G A C C C T C T
 SEQ. ID. NO. 21 T G T G T A T C C T G A T C T G C T G G C A G G C

SEQ. ID. NO. 18 C C T C T T T G C C G T G C T G G G C A T T T T T C
 SEQ. ID. NO. 19 A C A T G T C C G T T A T A T C C A G A A C T C A
 SEQ. ID. NO. 20 G C A C C G G A C C A T T G A G A C A T T T G C C
 SEQ. ID. NO. 21 T G T G G A C C C C C T G C G A A G G A C A G T G

SEQ. ID. NO. 18 C T G A C A G C C T T T G T G C T G G G T G T G T
 SEQ. ID. NO. 19 C A G C C C A A C C T G A A C A A C C T G A C T G
 SEQ. ID. NO. 20 A A G G A G G A A C C T A A G G A A G A T A T T G
 SEQ. ID. NO. 21 G A G A A G T A C A G C A T G G A G C C G G A C C

SEQ. ID. NO. 18 T T A T C A A G T T C C G C A A C A C A C C C A T
 SEQ. ID. NO. 19 C T G T G G G C T G C T C A C T G G C T T T A G C
 SEQ. ID. NO. 20 A C G T C T C T A T T C T G C C C C A G C T G G A
 SEQ. ID. NO. 21 C A G C A G G A C G G G A T A T C T C C A T C C G

SEQ. ID. NO. 18 T G T C A A G G C C A C C A A C C G A G A G C T C
 SEQ. ID. NO. 19 T G C T G T C T T C C C C C T G G G G C T C G A T
 SEQ. ID. NO. 20 G C A T T G C A G C T C C A G G A A G A T G A A T
 SEQ. ID. NO. 21 C C C T C T C C T G G A G C A C T G T G A G A A C

SEQ. ID. NO. 18 T C C T A C C T C C T C C T C T T C T C C C T G C
 SEQ. ID. NO. 19 G G T T A C C A C A T T G G G A G G A A C C A G T
 SEQ. ID. NO. 20 A C A T G G C T T G G C A T T T T C T A T G G T T
 SEQ. ID. NO. 21 A C C C A T A T G A C C A T C T G G C T T G G C A

SEQ. ID. NO. 18 T C T G C T G C T T C T C C A G C T C C C T G T T
 SEQ. ID. NO. 19 T T C C T T T C G T C T G C C A G G C C C G C C T
 SEQ. ID. NO. 20 A C A A G G G G C T G C T G C T G C T G C T G G G
 SEQ. ID. NO. 21 T C G T C T A T G C C T A C A A G G G A C T T C T

Figure 5J

SEQ. ID. NO. 18 C T T C A T C G G G G A G C C C C A G G A C T G G
 SEQ. ID. NO. 19 C T G G C T C C T G G G C C T G G G C T T T A G T
 SEQ. ID. NO. 20 A A T C T T C C T T G C T T A T G A G A C C A A G
 SEQ. ID. NO. 21 C A T G T T G T T C G G T T G T T T C T T A G C T

SEQ. ID. NO. 18 A C G T G C C G C C T G C G C C A G C C G G C C T
 SEQ. ID. NO. 19 C T G G G C T A C G G T T C C A T G T T C A C C A
 SEQ. ID. NO. 20 A G T G T G T C C A C T G A G A A G A T C A A T G
 SEQ. ID. NO. 21 T G G G A G A C C C G C A A C G T C A G C A T C C

SEQ. ID. NO. 18 T T G G C A T C A G C T T C G T G C T C T G C A T
 SEQ. ID. NO. 19 A G A T T T G G T G G G T C C A C A C G G T C T T
 SEQ. ID. NO. 20 A T C A C C G G G C T G T G G G C A T G G C T A T
 SEQ. ID. NO. 21 C C G C A C T C A A C G A C A G C A A G T A C A T

SEQ. ID. NO. 18 C T C A T G C A T C C T G G T G A A A A C C A A C
 SEQ. ID. NO. 19 C A C A A A G A A A G G A A G A A A A G A A G G A G
 SEQ. ID. NO. 20 C T A C A A T G T G G C A G T C C T G T G C C T C
 SEQ. ID. NO. 21 C G G G A T G A G T G T C T A C A A C G T G G G G

SEQ. ID. NO. 18 C G T G T C C T C C T G G T G T T T G A G G C C A
 SEQ. ID. NO. 19 T G G A G G A A G A C T C T G G A A C C C T G G A
 SEQ. ID. NO. 20 A T C A C T G C T C C T G T C A C C A T G A T T C
 SEQ. ID. NO. 21 A T C A T G T G C A T C A T C G G G G C C G C T G

SEQ. ID. NO. 18 A G A T C C C C A C C A G C T T C C A C C G C A A
 SEQ. ID. NO. 19 A G C T G T A T G C C A C A G T G G G C C T G C T
 SEQ. ID. NO. 20 T G T C C A G C C A G C A G G A T G C A G C C T T
 SEQ. ID. NO. 21 T C T C C T T C C T G A C C C G G G A C C A G C C

SEQ. ID. NO. 18 G T G G T G G G G G C T C A A C C T G C A G T T C
 SEQ. ID. NO. 19 G G T G G G C A T G G A T G T C C T C A C T C T C
 SEQ. ID. NO. 20 T G C C T T T G C C T C T C T T G C C A T A G T T
 SEQ. ID. NO. 21 C A A T G T G C A G T T C T G C A T C G T G G C T

SEQ. ID. NO. 18 C T G C T G G T T T T C C T C T G C A C C T T C A
 SEQ. ID. NO. 19 G C C A T C T G G C A G A T C G T G G A C C C T C
 SEQ. ID. NO. 20 T T C T C C T C C T A T A T C A C T C T T G T T G
 SEQ. ID. NO. 21 C T G G T C A T C A T C T T C T G C A G C A C C A

Figure 5k

SEQ. ID. NO. 18 T G C A G A T T G T C A T C T G T G T G A T C T G
 SEQ. ID. NO. 19 T G C A C C G G A C C A T T G A G A C A T T T G C
 SEQ. ID. NO. 20 T G C T C T T T G T G C C C A A G A T G C G C A G
 SEQ. ID. NO. 21 T C A C C C T C T G C C T G G T A T T C G T G C C

SEQ. ID. NO. 18 G C T C T A C A C C G C G C C C C C C T C A A G C
 SEQ. ID. NO. 19 C A A G G A G G A A C C T A A G G A A G A T A T T
 SEQ. ID. NO. 20 G C T G A T C A C C C G A G G G G A A T G G C A G
 SEQ. ID. NO. 21 G A A G C T C A T C A C C C T G A G A A C A A A C

SEQ. ID. NO. 18 T A C C G C A A C C A G G A G C T G G A G G A T G
 SEQ. ID. NO. 19 G A C G T C T C T A T T C T G C C C C A G C T G G
 SEQ. ID. NO. 20 T C G G A G G C G C A G G A C A C C A T G A A G A
 SEQ. ID. NO. 21 C C A G A T G C A G C A A C G C A G A A C A G G C

SEQ. ID. NO. 18 A G A T C A T C T T C A T C A C G T G C C A C G A
 SEQ. ID. NO. 19 A G C A T T G C A G C T C C A G G A A G A T G A A
 SEQ. ID. NO. 20 C A G G G T C A T C G A C C A A C A A C A A C G A
 SEQ. ID. NO. 21 G A T T C C A G T T C A C T C A G A A T C A G A A

SEQ. ID. NO. 18 G G G C T C C C T C A T G G C C C T G G G C T T C
 SEQ. ID. NO. 19 T A C A T G G C T T G G C A T T T T C T A T G G T
 SEQ. ID. NO. 20 G G A G G A G A A G T C C C G G C T G T T G G A G
 SEQ. ID. NO. 21 G A A A G A A G A T T C T A A A A C G T C C A C C

SEQ. ID. NO. 18 C T G A T C G G C T A C A C C T G C C T G C T G G
 SEQ. ID. NO. 19 T A C A A G G G G C T G C T G C T G C T G C T G G
 SEQ. ID. NO. 20 A A G G A G A A C C G T G A A C T G G A A A A G A
 SEQ. ID. NO. 21 T C G G T C A C C A G T G T G A A C C A A G C C A

SEQ. ID. NO. 18 C T G C C A T C T G C T T C T T C T T T G C C T T
 SEQ. ID. NO. 19 G A A T C T T C C T T G C T T A T G A G A C C A A
 SEQ. ID. NO. 20 T C A T T G C T G A G A A A G A G G A G C G T G T
 SEQ. ID. NO. 21 G C A C A T C C C G C C T G G A G G G C C T A C A

SEQ. ID. NO. 18 C A A G T C C C G G A A G C T G C C G G A G A A C
 SEQ. ID. NO. 19 G A G T G T G T C C A C T G A G A A G A T C A A T
 SEQ. ID. NO. 20 C T C T G A A C T G C G C C A T C A A C T C C A G
 SEQ. ID. NO. 21 G T C A G A A A A C C A T C G C C T G C G A A T G

Figure 51

SEQ. ID. NO. 18 T T C A A T G A A G C C A A G T T C A T C A C C T
 SEQ. ID. NO. 19 G A T C A C C G G G C T G T G G G C A T G G C T A
 SEQ. ID. NO. 20 T C T C G G C A G C A G C T C C G C T C C C G G C
 SEQ. ID. NO. 21 A A G A T C A C A G A G C T G G A T A A A G A C T

SEQ. ID. NO. 18 T C A G C A T G C T C A T C T T C T T C A T C G T
 SEQ. ID. NO. 19 T C T A C A A T G T G G C A G T C C T G T G C C T
 SEQ. ID. NO. 20 G C C A C C C A C C G A C A C C C C C A G A A C C
 SEQ. ID. NO. 21 T G G A A G A G G T C A C C A T G C A G C T G C A

SEQ. ID. NO. 18 C T G G A T C T C C T T C A T T C C A G C C T A T
 SEQ. ID. NO. 19 C A T C A C T G C T C C T G T C A C C A T G A T T
 SEQ. ID. NO. 20 C T C T G G G G G C C T G C C C A G G G G A C C C
 SEQ. ID. NO. 21 G G A C A C A C C A G A A A A G A C C A C C T A C

SEQ. ID. NO. 18 G C C A G C A C C T A T G G C A A G T T T G T C T
 SEQ. ID. NO. 19 C T G T C C A G C C A G C A G G A T G C A G C C T
 SEQ. ID. NO. 20 C C T G A G C C C C C C G A C C G G C T T A G C T
 SEQ. ID. NO. 21 A T T A A A C A G A A C C A C T A C C A A G A G C

SEQ. ID. NO. 18 C T G C C G T A G A G G T G A T T G C C A T C C T
 SEQ. ID. NO. 19 T T G C C T T T G C C T C T C T T G C C A T A G T
 SEQ. ID. NO. 20 G T G A T G G G A G T C G A G T G C A T T T G C T
 SEQ. ID. NO. 21 T C A A T G A C A T C C T C A A C C T G G G A A A

SEQ. ID. NO. 18 G G C A G C C A G C T T T G G C T T G C T G G C G
 SEQ. ID. NO. 19 T T T C T C C T C C T A T A T C A C T C T T G T T
 SEQ. ID. NO. 20 T T A T A A G T G A G G G T A G G G T G A G G G A
 SEQ. ID. NO. 21 C T T C A C T G A G A G C A C A G A T G G A G G A

SEQ. ID. NO. 18 T G C A T C T T C T T C A A C A A G A T C T A C A
 SEQ. ID. NO. 19 G T G C T C T T T G T G C C C A A G A T G C G C A
 SEQ. ID. NO. 20 G G A C A G G C C A G T A G G G G G A G G G A A A
 SEQ. ID. NO. 21 A A G G C C A T T T T A A A A A A T C A C C T C G

SEQ. ID. NO. 18 T C A T T C T C T T C A A G C C A T C C C G C A A
 SEQ. ID. NO. 19 G G C T G A T C A C C C G A G G G G A A T G G C A
 SEQ. ID. NO. 20 G G G A G A G G G G A A G G G C A G G G A C T C
 SEQ. ID. NO. 21 A T C A A A A T C C C C A G C T A C A G T G G A A

Figure 5m

SEQ. ID. NO. 18 C A C C A T C G A G G A G G T G C G T T G C A G C
 SEQ. ID. NO. 19 G T C G G A G G C G C A G G A C A C C A T G A A G
 SEQ. ID. NO. 20 A G G A A G C A G G G G G T C C C C A T C C C C A
 SEQ. ID. NO. 21 C A C A A C A G A G C C C T C T C G A A C A T G C

SEQ. ID. NO. 18 A C C G C A G C T C A C G C T T T C A A G G T G G
 SEQ. ID. NO. 19 A C A G G G T C A T C G A C C A A C A A C A A C G
 SEQ. ID. NO. 20 G C T G G G A A G A A C A T G C T A T C C A A T C
 SEQ. ID. NO. 21 A A A G A T C C T A T A G A A G A T A T A A A C T

SEQ. ID. NO. 18 C T G C C C G G G C C A C G C T G C G C C G C A G
 SEQ. ID. NO. 19 A G G A G G A G A A G T C C C G G C T G T T G G A
 SEQ. ID. NO. 20 T C A T C T C T T G T A A A T A C A T G T C C C C
 SEQ. ID. NO. 21 C T C C A G A A C A C A T C C A G C G T C G G C T

SEQ. ID. NO. 18 C A A C G T C T C C C G C A A G C G G T C C A G C
 SEQ. ID. NO. 19 G A A G G A G A A C C G T G A A C T G G A A A A G
 SEQ. ID. NO. 20 C T G T G A G T T C T G G G C T G A T T T G G G T
 SEQ. ID. NO. 21 G T C C C T C C A G C T C C C C A T C C T C C A C

SEQ. ID. NO. 18 A G C C T T G G A G G C T C C A C G G G A T C C A
 SEQ. ID. NO. 19 A T C A T T G C T G A G A A A G A G G A G C G T G
 SEQ. ID. NO. 20 C T C T C A T A C C T C T G G G A A A C A G A C C
 SEQ. ID. NO. 21 C A C G C C T A C C T C C C A T C C A T C G G A G

SEQ. ID. NO. 18 C C C C C T C C T C C T C C A T C A G C A G C A A
 SEQ. ID. NO. 19 T C T C T G A A C T G C G C C A T C A G C T C C A
 SEQ. ID. NO. 20 T T T T T C T C T C T T A C T G C T T C A T G T A
 SEQ. ID. NO. 21 G C G T G G A C G C C A G C T G T G T C A G C C C

SEQ. ID. NO. 18 G A G C A A C A G C G A A G A C C C A T T C C C A
 SEQ. ID. NO. 19 G T C T C G G C A G C A G C T C C G C T C C C G G
 SEQ. ID. NO. 20 A T T T T G T A T C A C C T C T T C A C A A T T T
 SEQ. ID. NO. 21 C T G C G T C A G C C C C A C C G C C A G C C C C

SEQ. ID. NO. 18 C A G C C C G A G A G G C A G A A G C A G C A G C
 SEQ. ID. NO. 19 C G C C A C C C A C C G A C A C C C C C A G A A C
 SEQ. ID. NO. 20 A G T T C G T A C C T G G C T T G A A G C T G C T
 SEQ. ID. NO. 21 C G C C A C A G A C A T G T G C C A C C C T C C T

Figure 5n

SEQ. ID. NO. 18 A G C C G C T G G C C C T A A C C C A G C A A G A
 SEQ. ID. NO. 19 C C T C T G G G G G C C T G C C C A G G G G A C C
 SEQ. ID. NO. 20 C A C T G C T C A C A C G C T G C C T C C T C A G
 SEQ. ID. NO. 21 T C C G A G T C A T G G T C T C G G G C C T G T A

SEQ. ID. NO. 18 G C A G C A G C A G C A G C C C C T G A C C C T C
 SEQ. ID. NO. 19 C C C T G A G C C C C C G A C C G G C T T A G C
 SEQ. ID. NO. 20 C A G C C T C A C T G C A T C T T T C T C T T C C
 SEQ. ID. NO. 21 A G G G T G G G A G G C C T G G G C C C G G G G C

SEQ. ID. NO. 18 C C A C A G C A G C A A C G A T C T C A G C A G C
 SEQ. ID. NO. 19 T G T G A T G G G A G T C G A G T G C A T T T G C
 SEQ. ID. NO. 20 C A T G C A A C A C C C T C T T C T A G T T A C C
 SEQ. ID. NO. 21 C T C C C C C G T G A C A G A A C C A C A C T G G

SEQ. ID. NO. 18 A G C C C A G A T G C A A G C A G A A G G T C A T
 SEQ. ID. NO. 19 T T T A T A A G T G A G G G T A G G G T G A G G G
 SEQ. ID. NO. 20 A C G G C A A C C C C T
 SEQ. ID. NO. 21 G C A G A G G G G T C T G C T G C A G A A A C A C

SEQ. ID. NO. 18 C T T T G G C A G C G G C A C G G T C A C C T T C
 SEQ. ID. NO. 19 A G G A C A G G C C A G T A G G G G G A G G G A A
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 T G T C G G C T C T G G C T G C G G A G A A G C T

SEQ. ID. NO. 18 T C A C T G A G C T T T G A T G A G C C T C A G A
 SEQ. ID. NO. 19 A G G G A G A G G G G A A G G G C A G G G G A C T
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 G G G C A C C A T G G C T G G C C T C T C A G G A

SEQ. ID. NO. 18 A G A A C G C C A T G G C C C A C G G G A A T T C
 SEQ. ID. NO. 19 C A G G A A G C A G G G G G T C C C C A T C C C C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 C C A C T C G G A T G G C A C T C A G G T G G A C

SEQ. ID. NO. 18 T A C G C A C C A G A A C T C C C T G G A G G C C
 SEQ. ID. NO. 19 A G C T G G G A A G A A C A T G C T A T C C A A T
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A G G A C G G G G C A G G G G G A G A C T T G G C

Figure 5o

SEQ. ID. NO. 18 C A G A A A A G C A G C G A T A C G C T G A C C C
 SEQ. ID. NO. 19 C T C A T C T C T T G T A A A T A C A T G T C C C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A C C T G A C C T C G A G C C T T A T T T G T G A

SEQ. ID. NO. 18 G A C A C C A G C C A T T A C T C C C G C T G C A
 SEQ. ID. NO. 19 C C T G T G A G T T C T G G G C T G A T T T G G G
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A G T C C T T A T T T C T T C A C A A G A A G A

SEQ. ID. NO. 18 G T G C G G G G A A A C G G A C T T A G A T C T G
 SEQ. ID. NO. 19 T C T C T C A T A C C T C T G G G A A A C A G A C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 G G A A C G G A A A T G G G A C G T C T T C C T T

SEQ. ID. NO. 18 A C C G T C C A G G A A A C A G G T C T G C A A G
 SEQ. ID. NO. 19 C T T T T T C T C T C T T A C T G C T T C A T G T
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A A C A T C T G C A A A C A A G G A G G C G C T G

SEQ. ID. NO. 18 G A C C T G T G G G T G G A G A C C A G C G G C C
 SEQ. ID. NO. 19 A A T T T T G T A T C A C C T C T T C A C A A T T
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 G G A T A T C A A A C T T G C A A A A A A A A A A

SEQ. ID. NO. 18 A G A G G T G G A G G A C C C T G A A G A G T T G
 SEQ. ID. NO. 19 T A G T T C G T A C C T G G C T T G A A G C T G C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21 A A A A A A A A A A A A

SEQ. ID. NO. 18 T C C C C A G C A C T T G T A G T G T C C A G T T
 SEQ. ID. NO. 19 T C A C T G C T C A C A C G C T G C C T C C T C A
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21

SEQ. ID. NO. 18 C A C A G A G C T T T G T C A T C A G T G G T G G
 SEQ. ID. NO. 19 G C A G C C T C A C T G C A T C T T T C T C T T C
 SEQ. ID. NO. 20
 SEQ. ID. NO. 21

Figure 5p

SEQ. ID. NO. 18 A G G C A G C A C T G T T A C A G A A A C G T A
SEQ. ID. NO. 19 C C A T G C A A C A C C C T C T T C T A G T T A C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18 G T G A A T T C A
SEQ. ID. NO. 19 C A C G G C A A C C C C T G C A G C T C C T C T G
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C T T T G T G C T C T G T T C C T G T C C A G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 A G G G G T C T C C C A A C A A G T G C T C T T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C A C C C C A A A G G G G C C T C T C C T T T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C T C C A C T G T C A T A A T C T C T T T C C A T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C T T A C T T G C C C T T C T A T A C T T T C T C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 A C A T G T G G C T C C C C C T G A A T T T T G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

Figure 5q

SEQ. ID. NO. 18
SEQ. ID. NO. 19 T T C C T T T G G G G A G C T C A T T C T T T C G
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C A A G G T C A C A T G C T C C C T T G C C T C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 T G G C T C C G T G C A
SEQ. ID. NO. 20
SEQ. ID. NO. 21

Figure 5r

FIGURE 6a

SEQ. ID. NO. 22 A T G C T G C T G C T G C T G C T G G T G C C T C T C T T C
SEQ. ID. NO. 23 A T G G G C C C G G G G G G A C C C T G T A C C C C A G T G

SEQ. ID. NO. 22 C T C C G C C C C C T G G G C G C T G G C G G G G C G C A G
SEQ. ID. NO. 23 G G G T G G C C G C T G C C T C T T C T G C T G G T G A T G

SEQ. ID. NO. 22 A C C C C C A A C G C C A C C T C G G A A G G T T G C C A G
SEQ. ID. NO. 23 G C G G C T G G G G T G G C T C C G G T G T G G G C C T C T

SEQ. ID. NO. 22 A T T A T A C A T C C G C C C T G G G A A G G T G G C A T C
SEQ. ID. NO. 23 C A C T C C C C T C A T C T C C C G C G G C C T C A C C C G

SEQ. ID. NO. 22 A G G T A C C G T G G C T T G A C T C G C G A C C A G G T G
SEQ. ID. NO. 23 A G G G T C C C C C C G C A C C C C T C C T C A G A A C G G

SEQ. ID. NO. 22 A A G G C C A T C A A C T T C C T G C C T G T G G A C T A T
SEQ. ID. NO. 23 C G T G C A G T A T A C A T C G G G G C G C T G T T T C C C

SEQ. ID. NO. 22 G A G A T C G A A T A T G T G T G C C G A G G G G A G C G C
SEQ. ID. NO. 23 A T G A G C G G G G G C T G G C C G G G G G C C A G G C C

SEQ. ID. NO. 22 G A G G T G G T G G G G C C C A A G G T G C G C A A A T G C
SEQ. ID. NO. 23 T G C C A G C C C G C G G T G G A G A T G G C G C T G G A G

SEQ. ID. NO. 22 C T G G C C A A C G G C T C C T G G A C G G A T A T G G A C
SEQ. ID. NO. 23 G A C G T T A A C A G C C G C A G A G A C A T C C T G C C G

SEQ. ID. NO. 22 A C A C C C A G C C G C T G T G T C C G A A T C T G C T C C
SEQ. ID. NO. 23 G A C T A C G A G C T C A A G C T T A T C C A C C A C G A C

SEQ. ID. NO. 22 A A G T C T T A T T T G A C C C T G G A A A A T G G G A A G
SEQ. ID. NO. 23 A G C A A G T G T G A C C C A G G G C A A G C C A C C A A G

SEQ. ID. NO. 22 G T T T T C C T G A C G G G T G G G G A C C T C C C A G C T
SEQ. ID. NO. 23 T A C T T G T A C G A A C T A C T C T A C A A T G A C C C C

FIGURE 6b

SEQ. ID. NO. 22 C T G G A T G G A G C C C G G G T G G A G T T C C G A T G T
SEQ. ID. NO. 23 A T C A A G A T C A T T C T C A T G C C T G G C T G T A G T

SEQ. ID. NO. 22 G A C C C C G A C T T C C A T C T G G T G G G C A G C T C C
SEQ. ID. NO. 23 T C T G T C T C C A C A C T T G T A G C T G A G G C T G C C

SEQ. ID. NO. 22 C G G A G C G T C T G T A G T C A G G G C C A G T G G A G C
SEQ. ID. NO. 23 C G G A T G T G G A A C C T T A T T G T G C T C T C A T A T

SEQ. ID. NO. 22 A C C C C C A A G C C C C A C T G C C A G G T G A A T C G A
SEQ. ID. NO. 23 G G C T C C A G T T C A C C A G C C T T G T C A A A C C G A

SEQ. ID. NO. 22 A C G C C A C A C T C A G A A C G G C G T G C A G T A T A C
SEQ. ID. NO. 23 C A G C G G T T T C C C A C G T T C T T C C G G A C G C A T

SEQ. ID. NO. 22 A T C G G G G C G C T G T T T C C C A T G A G C G G G G G C
SEQ. ID. NO. 23 C C A T C C G C C A C A C T C C A C A A T C C C A C C C G G

SEQ. ID. NO. 22 T G G C C G G G G G G C C A G G C C T G C C A G C C C G C G
SEQ. ID. NO. 23 G T G A A A C T C T T C G A A A A G T G G G G C T G G A A G

SEQ. ID. NO. 22 G T G G A G A T G G C G C T G G A G G A C G T T A A C A G C
SEQ. ID. NO. 23 A A G A T C G C T A C C A T C C A A C A G A C C A C C G A G

SEQ. ID. NO. 22 C G C A G A G A C A T C C T G C C G G A C T A C G A G C T C
SEQ. ID. NO. 23 G T C T T C A C C T C A A C G C T G G A T G A C C T G G A G

SEQ. ID. NO. 22 A A G C T T A T C C A C C A C G A C A G C A A G T G T G A C
SEQ. ID. NO. 23 G A G C G A G T G A A A G A G G C T G G G A T C G A G A T C

SEQ. ID. NO. 22 C C A G G G C A A G C C A C C A A G T A C T T G T A C G A A
SEQ. ID. NO. 23 A C T T T C C G A C A G A G T T T C T T C T C G G A T C C A

SEQ. ID. NO. 22 C T A C T C T A C A A T G A C C C C A T C A A G A T C A T T
SEQ. ID. NO. 23 G C T G T G C C T G T T A A A A A C C T G A A G C G T C A A

SEQ. ID. NO. 22 C T C A T G C C T G G C T G T A G T T C T G T C T C C A C A
SEQ. ID. NO. 23 G A T G C T C G A A T C A T C G T G G G A C T T T T C T A T

FIGURE 6c

SEQ. ID. NO. 22 C T T G T A G C T G A G G C T G C C C G G A T G T G G A A C
SEQ. ID. NO. 23 G A G A C G G A A G C C C G G A A A G T T T T T T G T G A G

SEQ. ID. NO. 22 C T T A T T G T G C T C T C A T A T G G C T C C A G T T C A
SEQ. ID. NO. 23 G T C T A T A A G G A A A G G C T C T T T G G G A A G A A G

SEQ. ID. NO. 22 C C A G C C T T G T C A A A C C G A C A G C G G T T T C C C
SEQ. ID. NO. 23 T A C G T C T G G T T C C T C A T C G G G T G G T A T G C T

SEQ. ID. NO. 22 A C G T T C T T C C G G A C G C A T C C A T C C G C C A C A
SEQ. ID. NO. 23 G A C A A C T G G T T C A A G A C C T A T G A C C C G T C A

SEQ. ID. NO. 22 C T C C A C A A T C C C A C C C G G G T G A A A C T C T T C
SEQ. ID. NO. 23 A T C A A T T G T A C A G T G G A A G A A A T G A C C G A G

SEQ. ID. NO. 22 G A A A A G T G G G G C T G G A A G A A G A T C G C T A C C
SEQ. ID. NO. 23 G C G G T G G A G G G C C A C A T C A C C A C G G A G A T T

SEQ. ID. NO. 22 A T C C A A C A G A C C A C C G A G G T C T T C A C C T C A
SEQ. ID. NO. 23 G T C A T G C T G A A C C C T G C C A A C A C C C G A A G C

SEQ. ID. NO. 22 A C G C T G G A T G A C C T G G A G G A G C G A G T G A A A
SEQ. ID. NO. 23 A T T T C C A A C A T G A C G T C A C A G G A A T T T G T G

SEQ. ID. NO. 22 G A G G C T G G G A T C G A G A T C A C T T T C C G A C A G
SEQ. ID. NO. 23 G A G A A A C T A A C C A A G C G G C T G A A A A G A C A C

SEQ. ID. NO. 22 A G T T T C T T C T C G G A T C C A G C T G T G C C T G T T
SEQ. ID. NO. 23 C C C G A G G A G A C T G G A G G C T T C C A G G A G G C A

SEQ. ID. NO. 22 A A A A A C C T G A A G C G T C A A G A T G C T C G A A T C
SEQ. ID. NO. 23 C C A C T G G C C T A T G A T G C T A T C T G G G C C T T G

SEQ. ID. NO. 22 A T C G T G G G A C T T T T C T A T G A G A C G G A A G C C
SEQ. ID. NO. 23 G C T T T G G C C T T G A A C A A G A C G T C T G G A G G A

SEQ. ID. NO. 22 C G G A A A G T T T T T G T G A G G T C T A T A A G G A A
SEQ. ID. NO. 23 G G T G G T C G T T C C G G C G T G C G C C T G G A G G A C

FIGURE 6d

SEQ. ID. NO. 22 A G G C T C T T T G G G A A G A A G T A C G T C T G G T T C
SEQ. ID. NO. 23 T T T A A C T A C A A C A A C C A G A C C A T T A C A G A C

SEQ. ID. NO. 22 C T C A T C G G G T G G T A T G C T G A C A A C T G G T T C
SEQ. ID. NO. 23 C A G A T C T A C C G G G C C A T G A A C T C C T C C T C C

SEQ. ID. NO. 22 A A G A C C T A T G A C C C G T C A A T C A A T T G T A C A
SEQ. ID. NO. 23 T T T G A G G G C G T T T C T G G C C A T G T G G T C T T T

SEQ. ID. NO. 22 G T G G A A G A A A T G A C C G A G G C G G T G G A G G G C
SEQ. ID. NO. 23 G A T G C C A G C G G C T C C C G G A T G G C A T G G A C A

SEQ. ID. NO. 22 C A C A T C A C C A C G G A G A T T G T C A T G C T G A A C
SEQ. ID. NO. 23 C T T A T C G A G C A G C T A C A G G G C G G C A G C T A C

SEQ. ID. NO. 22 C C T G C C A A C A C C C G A A G C A T T T C C A A C A T G
SEQ. ID. NO. 23 A A G A A G A T C G G C T A C T A C G A C A G C A C C A A G

SEQ. ID. NO. 22 A C G T C A C A G G A A T T T G T G G A G A A A C T A A C C
SEQ. ID. NO. 23 G A T G A T C T T T C C T G G T C C A A A A C G G A C A A G

SEQ. ID. NO. 22 A A G C G G C T G A A A A G A C A C C C C G A G G A G A C T
SEQ. ID. NO. 23 T G G A T T G G A G G G T C T C C C C C A G C T G A C C A G

SEQ. ID. NO. 22 G G A G G C T T C C A G G A G G C A C C A C T G G C C T A T
SEQ. ID. NO. 23 A C C T T G G T C A T C A A G A C A T T C C G T T T C C T G

SEQ. ID. NO. 22 G A T G C T A T C T G G G C C T T G G C T T T G G C C T T G
SEQ. ID. NO. 23 T C T C A G A A A C T C T T T A T C T C C G T C T C A G T T

SEQ. ID. NO. 22 A A C A A G A C G T C T G G A G G A G G T G G T C G T T C C
SEQ. ID. NO. 23 C T C T C C A G C C T G G G C A T T G T T C T T G C T G T T

SEQ. ID. NO. 22 G G C G T G C G C C T G G A G G A C T T T A A C T A C A A C
SEQ. ID. NO. 23 G T C T G T C T G T C C T T T A A C A T C T A C A A C T C C

SEQ. ID. NO. 22 A A C C A G A C C A T T A C A G A C C A G A T C T A C C G G
SEQ. ID. NO. 23 C A C G T T C G T T A T A T C C A G A A C T C C C A G C C C

FIGURE 6e

SEQ. ID. NO. 22 G C C A T G A A C T C C T C C T C C T T T G A G G G C G T T
SEQ. ID. NO. 23 A A C C T G A A C A A T C T G A C T G C T G T G G G C T G C

SEQ. ID. NO. 22 T C T G G C C A T G T G G T C T T T G A T G C C A G C G G C
SEQ. ID. NO. 23 T C A C T G G C A C T G G C T G C T G T C T T C C C T C T C

SEQ. ID. NO. 22 T C C C G G A T G G C A T G G A C A C T T A T C G A G C A G
SEQ. ID. NO. 23 G G G C T G G A T G G T T A C C A C A T A G G G A G A A G C

SEQ. ID. NO. 22 C T A C A G G G C G G C A G C T A C A A G A A G A T C G G C
SEQ. ID. NO. 23 C A G T T C C C G T T T G T C T G C C A G G C C C G C C T T

SEQ. ID. NO. 22 T A C T A C G A C A G C A C C A A G G A T G A T C T T T C C
SEQ. ID. NO. 23 T G G C T C T T G G G C T T G G G C T T T A G T C T G G G C

SEQ. ID. NO. 22 T G G T C C A A A A C G G A C A A G T G G A T T G G A G G G
SEQ. ID. NO. 23 T A T G G C T C T A T G T T C A C C A A G A T C T G G T G G

SEQ. ID. NO. 22 T C T C C C C A G C T G A C C A G A C C T T G G T C A T C
SEQ. ID. NO. 23 G T C C A C A C A G T C T T C A C G A A G A A G G A G G A G

SEQ. ID. NO. 22 A A G A C A T T C C G T T T C C T G T C T C A G A A A C T C
SEQ. ID. NO. 23 A A G A A G G A G T G G A G G A A G A C C C T A G A G C C C

SEQ. ID. NO. 22 T T T A T C T C C G T C T C A G T T C T C T C C A G C C T G
SEQ. ID. NO. 23 T G G A A A C T C T A T G C C A C T G T G G G C C T G C T G

SEQ. ID. NO. 22 G G C A T T G T T C T T G C T G T T G T C T G T C T G T C C
SEQ. ID. NO. 23 G T G G G C A T G G A T G T C C T G A C T C T T G C C A T C

SEQ. ID. NO. 22 T T T A A C A T C T A C A A C T C C C A C G T T C G T T A T
SEQ. ID. NO. 23 T G G C A G A T T G T G G A C C C C T T G C A C C G A A C C

SEQ. ID. NO. 22 A T C C A G A A C T C C C A G C C C A A C C T G A A C A A T
SEQ. ID. NO. 23 A T T G A G A C T T T T G C C A A G G A G G A A C C A A A G

SEQ. ID. NO. 22 C T G A C T G C T G T G G G C T G C T C A C T G G C A C T G
SEQ. ID. NO. 23 G A A G A C A T C G A T G T C T C C A T T C T G C C C C A G

FIGURE 6f

SEQ. ID. NO. 22 G C T G C T G T C T T C C C T C T C G G G C T G G A T G G T
SEQ. ID. NO. 23 T T G G A G C A C T G C A G C T C C A A G A A G A T G A A T

SEQ. ID. NO. 22 T A C C A C A T A G G G A G A A G C C A G T T C C C G T T T
SEQ. ID. NO. 23 A C G T G G C T T G G C A T T T T C T A T G G T T A C A A G

SEQ. ID. NO. 22 G T C T G C C A G G C C C G C C T T T G G C T C T T G G G C
SEQ. ID. NO. 23 G G G C T G C T G C T G C T G C T G G G A A T C T T T C T T

SEQ. ID. NO. 22 T T G G G C T T T A G T C T G G G C T A T G G C T C T A T G
SEQ. ID. NO. 23 G C T T A C G A A A C C A A G A G C G T G T C C A C T G A A

SEQ. ID. NO. 22 T T C A C C A A G A T C T G G T G G G T C C A C A C A G T C
SEQ. ID. NO. 23 A A G A T C A A T G A C C A C A G G G C C G T G G G C A T G

SEQ. ID. NO. 22 T T C A C G A A G A A G G A G G A G A A G A A G G A G T G G
SEQ. ID. NO. 23 G C T A T C T A C A A T G T C G C G G T C C T G T G T C T C

SEQ. ID. NO. 22 A G G A A G A C C C T A G A G C C C T G G A A A C T C T A T
SEQ. ID. NO. 23 A T C A C T G C T C C T G T G A C C A T G A T C C T T T C C

SEQ. ID. NO. 22 G C C A C T G T G G G C C T G C T G G T G G G C A T G G A T
SEQ. ID. NO. 23 A G T C A G C A G G A C G C A G C C T T T G C C T T T G C C

SEQ. ID. NO. 22 G T C C T G A C T C T T G C C A T C T G G C A G A T T G T G
SEQ. ID. NO. 23 T C T C T G G C C A T C G T G T T C T C T T C C T A C A T C

SEQ. ID. NO. 22 G A C C C C T T G C A C C G A A C C A T T G A G A C T T T T
SEQ. ID. NO. 23 A C T C T G G T T G T G C T C T T T G T G C C C A A G A T G

SEQ. ID. NO. 22 G C C A A G G A G G A A C C A A A G G A A G A C A T C G A T
SEQ. ID. NO. 23 C G C A G G C T G A T C A C C C G A G G G G A A T G G C A G

SEQ. ID. NO. 22 G T C T C C A T T C T G C C C C A G T T G G A G C A C T G C
SEQ. ID. NO. 23 T C T G A A A C G C A G G A C A C C A T G A A A A C A G G A

SEQ. ID. NO. 22 A G C T C C A A G A A G A T G A A T A C G T G G C T T G G C
SEQ. ID. NO. 23 T C A T C C A C C A A C A A C A A C G A G G A A G A G A A G

FIGURE 6c

SEQ. ID. NO. 22 A T T T T C T A T G G T T A C A A G G G G C T G C T G C T G
SEQ. ID. NO. 23 T C C C G A C T G T T G G A G A A G G A A A A C C G A G A A

SEQ. ID. NO. 22 C T G C T G G G A A T C T T T C T T G C T T A C G A A A C C
SEQ. ID. NO. 23 C T G G A A A A G A T C A T C G C T G A G A A A G A G G A G

SEQ. ID. NO. 22 A A G A G C G T G T C C A C T G A A A A G A T C A A T G A C
SEQ. ID. NO. 23 C G C G T C T C T G A A C T G C G C C A T C A G C T C C A G

SEQ. ID. NO. 22 C A C A G G G C C G T G G G C A T G G C T A T C T A C A A T
SEQ. ID. NO. 23 T C T C G G C A G C A A C T C C G C T C A C G G C G C C A C

SEQ. ID. NO. 22 G T C G C G G T C C T G T G T C T C A T C A C T G C T C C T
SEQ. ID. NO. 23 C C C C C A A C A C C C C C A G A T C C C T C T G G G G G C

SEQ. ID. NO. 22 G T G A C C A T G A T C C T T T C C A G T C A G C A G G A C
SEQ. ID. NO. 23 C T T C C C A G G G G A C C C T C T G A G C C C C C T G A C

SEQ. ID. NO. 22 G C A G C C T T T G C C T T T G C C T C T C T G G C C A T C
SEQ. ID. NO. 23 C G G C T T A G C T G T G A T G G G A G T C G A G T A C A T

SEQ. ID. NO. 22 G T G T T C T C T T C C T A C A T C A C T C T G G T T G T G
SEQ. ID. NO. 23 T T G C T T T A C A A G

SEQ. ID. NO. 22 C T C T T T G T G C C C A A G A T G C G C A G G C T G A T C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 A C C C G A G G G G A A T G G C A G T C T G A A A C G C A G
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A C A C C A T G A A A A C A G G A T C A T C C A C C A A C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 A A C A A C G A G G A A G A G A A G T C C C G A C T G T T G
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A G A A G G A A A A C C G A G A A C T G G A A A A G A T C
SEQ. ID. NO. 23

FIGURE 61.

SEQ. ID. NO. 22 A T C G C T G A G A A A G A G G A G C G C G T C T C T G A A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C T G C G C C A T C A G C T C C A G T C T C G G C A G C A A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C T C C G C T C A C G G C G C C A C C C C C C A A C A C C C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C C A G A T C C C T C T G G G G G C C T T C C C A G G G G A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C C C T C T G A G C C C C C T G A C C G G C T T A G C T G T
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A T G G G A G T C G A G T A C A T T T G C T T T A C A A G
SEQ. ID. NO. 23

FIGURE 7c

SEQ. ID. NO. 24 M L L L L L V P L F L R P L G A G G A Q T P N A T S E G C Q
 SEQ. ID. NO. 25 M G P G G P C T P V G W P L P L L L V M A A G V A P V W A S

SEQ. ID. NO. 24 I I H P P W E G G I R Y R G L T R D Q V K A I N F L P V D Y
 SEQ. ID. NO. 25 H S P H L P R P H P R V P P H P S S E R R A V Y I G A L F P

SEQ. ID. NO. 24 E I E Y V C R G E R E V V G P K V R K C L A N G S W T D M D
 SEQ. ID. NO. 25 M S G G W P G G Q A C Q P A V E M A L E D V N S R R D I L P

SEQ. ID. NO. 24 T P S R C V R I C S K S Y L T L E N G K V F L T G G D L P A
 SEQ. ID. NO. 25 D Y E L K L I H H D S K C D P G Q A T K Y L Y E L L Y N D P

SEQ. ID. NO. 24 L D G A R V E F R C D P D F H L V G S S R S V C S Q G Q W S
 SEQ. ID. NO. 25 I K I I L M P G C S S V S T L V A E A A R M W N L I V L S Y

SEQ. ID. NO. 24 T P K P H C Q V N R T P H S E R R A V Y I G A L F P M S G G
 SEQ. ID. NO. 25 G S S S P A L S N R Q R F P T F F R T H P S A T L H N P T R

SEQ. ID. NO. 24 W P G G Q A C Q P A V E M A L E D V N S R R D I L P D Y E L
 SEQ. ID. NO. 25 V K L F E K W G W K K I A T I Q Q T T E V F T S T L D D L E

SEQ. ID. NO. 24 K L I H H D S K C D P G Q A T K Y L Y E L L Y N D P I K I I
 SEQ. ID. NO. 25 E R V K E A G I E I T F R Q S F F S D P A V P V K N L K R Q

SEQ. ID. NO. 24 L M P G C S S V S T L V A E A A R M W N L I V L S Y G S S S
 SEQ. ID. NO. 25 D A R I I V G L F Y E T E A R K V F C E V Y K E R L F G K K

SEQ. ID. NO. 24 P A L S N R Q R F P T F F R T H P S A T L H N P T R V K L F
 SEQ. ID. NO. 25 Y V W F L I G W Y A D N W F K T Y D P S I N C T V E E M T E

SEQ. ID. NO. 24 E K W G W K K I A T I Q Q T T E V F T S T L D D L E E R V K
 SEQ. ID. NO. 25 A V E G H I T T E I V M L N P A N T R S I S N M T S Q E F V

SEQ. ID. NO. 24 E A G I E I T F R Q S F F S D P A V P V K N L K R Q D A R I
 SEQ. ID. NO. 25 E K L T K R L K R H P E E T G G F Q E A P L A Y D A I W A L

FIGURE 71

SEQ. ID. NO. 24 I V G L F Y E T E A R K V F C E V Y K E R L F G K K Y V W F
SEQ. ID. NO. 25 A L A L N K T S G G G G R S G V R L E D F N Y N N Q T I T D

SEQ. ID. NO. 24 L I G W Y A D N W F K T Y D P S I N C T V E E M T E A V E G
SEQ. ID. NO. 25 Q I Y R A M N S S S F E G V S G H V V F D A S G S R M A W T

SEQ. ID. NO. 24 H I T T E I V M L N P A N T R S I S N M T S Q E F V E K L T
SEQ. ID. NO. 25 L I E Q L Q G G S Y K K I G Y Y D S T K D D L S W S K T D K

SEQ. ID. NO. 24 K R L K R H P E E T G G F Q E A P L A Y D A I W A L A L A L
SEQ. ID. NO. 25 W I G G S P P A D Q I L V I K T F R F L S Q K L F I S V S V

SEQ. ID. NO. 24 N K T S G G G G R S G V R L E D F N Y N N Q T I T D Q I Y R
SEQ. ID. NO. 25 L S S L G I V L A V V C L S F N I Y N S H V R Y I Q N S Q P

SEQ. ID. NO. 24 A M N S S S F E G V S G H V V F D A S G S R M A W T L I E Q
SEQ. ID. NO. 25 N L N N L T A V G C S L A L A A V F P L G L D G Y H I G R S

SEQ. ID. NO. 24 L Q G G S Y K K I G Y Y D S T K D D L S W S K T D K W I G G
SEQ. ID. NO. 25 Q F P F V C Q A R L W L L G L G F S L G Y G S M F T K I W W

SEQ. ID. NO. 24 S P P A D Q I L V I K T F R F L S Q K L F I S V S V L S S L
SEQ. ID. NO. 25 V H T V F T K K E E K K E W R K T L E P W K L Y A T V G L L

SEQ. ID. NO. 24 G I V L A V V C L S F N I Y N S H V R Y I Q N S Q P N L N N
SEQ. ID. NO. 25 V G M D V L T L A I W Q I V D P L H R T I E T F A K E E P K

SEQ. ID. NO. 24 L T A V G C S L A L A A V F P L G L D G Y H I G R S Q F P F
SEQ. ID. NO. 25 E D I D V S I L P Q L E H C S S K K M N T W L G I F Y G Y K

SEQ. ID. NO. 24 V C Q A R L W L L G L G F S L G Y G S M F T K I W W V H T V
SEQ. ID. NO. 25 G L L L L L G I F L A Y E T K S V S T E K I N D H R A V G M

SEQ. ID. NO. 24 F T K K E E K K E W R K T L E P W K L Y A T V G L L V G M D
SEQ. ID. NO. 25 A I Y N V A V L C L I T A P V T M I L S S Q Q D A A F A F A

SEQ. ID. NO. 24 V L T L A I W Q I V D P L H R T I E T F A K E E P K E D I D
SEQ. ID. NO. 25 S L A I V F S S Y I T L V V L F V P K M R R L I T R G E W Q

FIGURE 7c

SEQ. ID. NO. 24 V S I L P Q L E H C S S K K M N T W L G I F Y G Y K G L L L
SEQ. ID. NO. 25 S E T Q D T M K T G S S T N N N E E E K S R L L E K E N R E

SEQ. ID. NO. 24 L L G I F L A Y E T K S V S T E K I N D H R A V G M A I Y N
SEQ. ID. NO. 25 L E K I I A E K E E R V S E L R H Q L Q S R Q Q L R S R R H

SEQ. ID. NO. 24 V A V L C L I T A P V T M I L S S Q Q D A A F A F A S L A I
SEQ. ID. NO. 25 P P T P P D P S G G L P R G P S E P P D R L S C D G S R V H

SEQ. ID. NO. 24 V F S S Y I T L V V L F V P K M R R L I T R G E W Q S E T Q
SEQ. ID. NO. 25 L L Y K

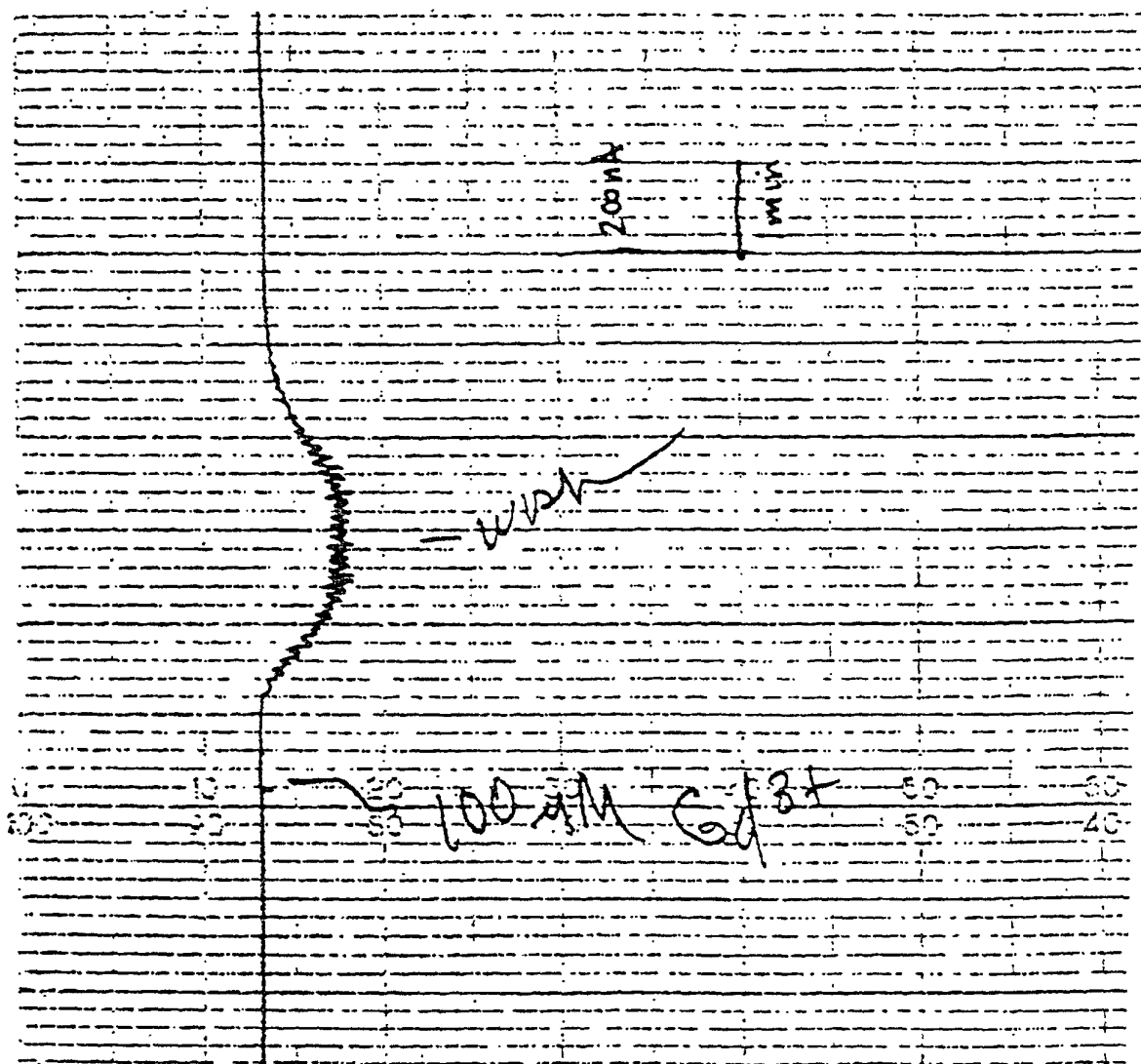
SEQ. ID. NO. 24 D T M K T G S S T N N N E E E K S R L L E K E N R E L E K I
SEQ. ID. NO. 25

SEQ. ID. NO. 24 I A E K E E R V S E L R H Q L Q S R Q Q L R S R R H P P T P
SEQ. ID. NO. 25

SEQ. ID. NO. 24 P D P S G G L P R G P S E P P D R L S C D G S R V H L L Y K
SEQ. ID. NO. 25

FIGURE 8

CHART NO. NZ 200 0



ClustalW Formatted Alignments

SEQ. ID. NO. 38 A T G G T A T G C G A G G G A A A G C G A T C A G
 SEQ. ID. NO. 34 A T G G G A T C G C T G C T T G C G C T C C C G G
 SEQ. ID. NO. 30 A T G G C A T T T T A T A G C T G C T G C T G G G
 SEQ. ID. NO. 26 A T G G G A T C G C T G C T T G C G C T C C T G G

SEQ. ID. NO. 38 C C T C T T G C C C T T G T T T C T T C C T C T T
 SEQ. ID. NO. 34 C A C T G C T G C T G C T G T G G G G T G C T G T
 SEQ. ID. NO. 30 T C C T C T T G G C A C T C A C C T G G C A C A C
 SEQ. ID. NO. 26 C A C T G C T G C C G C T G T G G G G T G C T G T

SEQ. ID. NO. 38 G A C C G C C A A G T T C T A C T G G A T C C T C
 SEQ. ID. NO. 34 G G C T G A G G G C C C A G C C A A G A A G G T G
 SEQ. ID. NO. 30 C T C T G C C T A C G G G C C A G A C C A G C G A
 SEQ. ID. NO. 26 G G C T G A G G G C C C A G C C A A G A A G G T G

SEQ. ID. NO. 38 A C A A T G A T G C A A A G A A C T C A C A G C C
 SEQ. ID. NO. 34 C T G A C C C T G G A G G G A G A C T T G G T G C
 SEQ. ID. NO. 30 G C C C A A A A G A A A G G G G G A C A T T A T C C
 SEQ. ID. NO. 26 C T G A C C C T G G A G G G A G A C T T G G T G C

SEQ. ID. NO. 38 A G G A G T A T G C C C A T T C C A T A C G G G T
 SEQ. ID. NO. 34 T G G G T G G G C T G T T C C C A G T G C A C C A
 SEQ. ID. NO. 30 T T G G G G G G C T C T T T C C T A T T C A T T T
 SEQ. ID. NO. 26 T G G G T G G G C T G T T C C C A G T G C A C C A

SEQ. ID. NO. 38 G G A T G G G G A C A T T A T T T T G G G G G G T
 SEQ. ID. NO. 34 G A A G G G C G G C C C A G C A G A G G A C T G T
 SEQ. ID. NO. 30 T G G A G T A G C A G C T A A A G A T C A A G A T
 SEQ. ID. NO. 26 G A A G G G C G G C C C A G C A G A G G A C T G T

SEQ. ID. NO. 38 C T C T T C C C T G T C C A C G C A A A G G G A G
 SEQ. ID. NO. 34 G G T C C T G T C A A T G A G C A C C G T G G C A
 SEQ. ID. NO. 30 C T C A A A T C A A A G G C C G G A G T C T G T G G
 SEQ. ID. NO. 26 G G T C C T G T C A A T G A G C A C C G T G G C A

SEQ. ID. NO. 38 A G A G A G G G G T G C C T T G T G G G G A G C T
 SEQ. ID. NO. 34 T C C A G C G C C T G G A G G C C A T G C T T T T
 SEQ. ID. NO. 30 A A T G T A T C A G G T A T A A T T T C C G T G G
 SEQ. ID. NO. 26 T C C A G C G C C T G G A G G C C A T G C T T T T

Figure 9a

SEQ. ID. NO. 38 G A A G A A G G A A A A G G G G A T T C A C A G A
 SEQ. ID. NO. 34 T G C A C T G G A C C G C A T C A A C C G T G A C
 SEQ. ID. NO. 30 G T T T C G C T G G T T A C A G G C T A T G A T A
 SEQ. ID. NO. 26 T G C A C T G G A C C G C A T C A A C C G T G A C

SEQ. ID. NO. 38 C T G G A G G C C A T G C T T T A T G C A A T T G
 SEQ. ID. NO. 34 C C G C A C C T G C T G C C T G G C G T G C G C C
 SEQ. ID. NO. 30 T T T G C C A T A G A G G A G A T A A A C A G C A
 SEQ. ID. NO. 26 C C G C A C C T G C T G C C T G G C G T G C G C C

SEQ. ID. NO. 38 A C C A G A T T A A C A A G G A C C C T G A T C T
 SEQ. ID. NO. 34 T G G G T G C A C A C A T C C T C G A C A G T T G
 SEQ. ID. NO. 30 G C C C A G C C C T T C T T C C C A A C T T G A C
 SEQ. ID. NO. 26 T G G G T G C A C A C A T C C T C G A C A G T T G

SEQ. ID. NO. 38 C C T T T C C A A C A T C A C T C T G G G T G T C
 SEQ. ID. NO. 34 C T C C A A G G A C A C A C A T G C G C T G G A G
 SEQ. ID. NO. 30 G C T G G G A T A C A G G A T A T T T G A C A C T
 SEQ. ID. NO. 26 C T C C A A G G A C A C A C A T G C G C T G G A G

SEQ. ID. NO. 38 C G C A T C C T C G A C A C G T G C T C T A G G G
 SEQ. ID. NO. 34 C A G G C A C T G G A C T T T G T G C G T G C C T
 SEQ. ID. NO. 30 T G C A A C A C C G T T T C T A A G G C C T T G G
 SEQ. ID. NO. 26 C A G G C A C T G G A C T T T G T G C G T G C C T

SEQ. ID. NO. 38 A C A C C T A T G C T T T T G G A G C A G T C T C T
 SEQ. ID. NO. 34 C A C T C A G C C G T G G T G C T G A T G G C T C
 SEQ. ID. NO. 30 A A G C C A C C C T G A G T T T T G T T G C T C A
 SEQ. ID. NO. 26 C A C T C A G C C G T G G T G C T G A T G G A T C

SEQ. ID. NO. 38 A A C A T T C G T G C A G G C A T T A A T A G A G
 SEQ. ID. NO. 34 A C G C C A C A T C T G C C C C G A C G G C T C T
 SEQ. ID. NO. 30 A A A C A A A A T T G A T T C T T T G A A C C T T
 SEQ. ID. NO. 26 A C G C C A C A T C T G C C C C G A C G G C T C T

SEQ. ID. NO. 38 A A A G A T G C T T C G G A T G T G A A G T G T G
 SEQ. ID. NO. 34 T A T G C G A C C C A T G G T G A T G C T C C C A
 SEQ. ID. NO. 30 G A T G A G T T C T G C A A C T G C T C A G A G C
 SEQ. ID. NO. 26 T A T G C G A C C C A T G G T G A T G C T C C C A

Figure 9b

SEQ. ID. NO. 38 C T A A T G G A G A T C C A C C C A T T T T C A C
 SEQ. ID. NO. 34 C T G C C A T C A C T G G T G T T A T T G G C G G
 SEQ. ID. NO. 30 A C A T T C C C T C T A C G A T T G C T G T G G T
 SEQ. ID. NO. 26 C T G C C A T C A C T G G T G T T A T T G G C G G

SEQ. ID. NO. 38 C A A G C C C G A C A A G A T T T C T G G C G T C
 SEQ. ID. NO. 34 T T C C T A C A G T G A T G T C T C C A T C C A G
 SEQ. ID. NO. 30 G G G A G C A A C T G G C T C A G G C G T C T C C
 SEQ. ID. NO. 26 T T C C T A C A G T G A T G T C T C C A T C C A G

SEQ. ID. NO. 38 A T A G G T G C T G C A G C A A G C T C C G T G T
 SEQ. ID. NO. 34 G T G G C C A A C C T C T T G A G G C T A T T T C
 SEQ. ID. NO. 30 A C G G C A G T G G C A A A T C T G C T G G G G C
 SEQ. ID. NO. 26 G T G G C C A A C C T C T T G A G G C T A T T T C

SEQ. ID. NO. 38 C C A T C A T G G T T G C T A A C A T T T T A A G
 SEQ. ID. NO. 34 A G A T C C C A C A G A T T A G C T A C G C C T C
 SEQ. ID. NO. 30 T C T T C T A C A T T C C C C A G G T C A G T T A
 SEQ. ID. NO. 26 A G A T C C C A C A G A T T A G C T A C G C C T C

SEQ. ID. NO. 38 A C T T T T T A A G A T A C C T C A A A T C A G C
 SEQ. ID. NO. 34 T A C C A G T G C C A A G C T G A G T G A C A A G
 SEQ. ID. NO. 30 T G C C T C C T C C A G C A G A C T C C T C A G C
 SEQ. ID. NO. 26 T A C C A G T G C C A A G C T G A G T G A C A A G

SEQ. ID. NO. 38 T A T G C A T C C A C A G C C C C A G A G C T A A
 SEQ. ID. NO. 34 T C C C G C T A T G A C T A C T T T G C C C G C A
 SEQ. ID. NO. 30 A A C A A G A A T C A A T T C A A G T C T T T C C
 SEQ. ID. NO. 26 T C C C G C T A T G A C T A C T T T G C C C G C A

SEQ. ID. NO. 38 G T G A T A A C A C C A G G T A T G A C T T T T T
 SEQ. ID. NO. 34 C A G T G C C T C C T G A C T T C T T C C A A G C
 SEQ. ID. NO. 30 T C C G A A C C A T C C C C A A T G A T G A G C A
 SEQ. ID. NO. 26 C A G T G C C T C C T G A C T T C T T C C A A G C

SEQ. ID. NO. 38 C T C T C G A G T G G T T C C G C C T G A C T C C
 SEQ. ID. NO. 34 C A A G G C C A T G G C T G A G A T T C T C C G C
 SEQ. ID. NO. 30 C C A G G C C A C T G C C A T G G C A G A C A T C
 SEQ. ID. NO. 26 C A A G G C C A T G G C T G A G A T T C T C C G C

Figure 9c

SEQ. ID. NO. 38 T A C C A A G C C C A A G C C A T G G T G G A C A
 SEQ. ID. NO. 34 T T C T T C A A C T G G A C C T A T G T G T C C A
 SEQ. ID. NO. 30 A T C G A G T A T T T C C G C T G G A A C T G G G
 SEQ. ID. NO. 26 T T C T T C A A C T G G A C C T A T G T G T C C A

SEQ. ID. NO. 38 T C G T G A C A G C A C T G G G A T G G A A T T A
 SEQ. ID. NO. 34 C T G T G G C G T C T G A G G G C G A C T A T G G
 SEQ. ID. NO. 30 T G G G C A C A A T T G C A G C T G A T G A C G A
 SEQ. ID. NO. 26 C T G A G G C C T C T G A G G G C G A C T A T G G

SEQ. ID. NO. 38 T G T T T C G A C A C T G G C T T C T G A G G G G
 SEQ. ID. NO. 34 C G A G A C A G G C A T T G A G G C C T T T G A G
 SEQ. ID. NO. 30 C T A T G G G C G G C C G G G A T T G A G A A A
 SEQ. ID. NO. 26 C G A G A C A G G C A T T G A G G C C T T T G A G

SEQ. ID. NO. 38 A A C T A T G G T G A G A G C G G T G T G G A G G
 SEQ. ID. NO. 34 C T A G A G G C T C G T G C C C G C A A C A T C T
 SEQ. ID. NO. 30 T T C C G A G A G G A A G C T G A G G A A A G G G
 SEQ. ID. NO. 26 C T A G A G G C T C G T G C C C G C A A C A T C T

SEQ. ID. NO. 38 C C T T C A C C C A G A T C T C G A G G G A G A T
 SEQ. ID. NO. 34 G T G T G G C C A C C T C G G A G A A A G T G G G
 SEQ. ID. NO. 30 A T A T C T G C A T C G A C T T C A G T G A A C T
 SEQ. ID. NO. 26 G T G T G G C C A C C T C G G A G A A A G T G G G

SEQ. ID. NO. 38 T G G T G G T G T T T G C A T T G C T C A G T C A
 SEQ. ID. NO. 34 C C G T G C C A T G A G C C G C G C G G C C T T T
 SEQ. ID. NO. 30 C A T C T C C C A G T A C T C T G A T G A G G A A
 SEQ. ID. NO. 26 C C G T G C C A T G A G C C G C G C G G C C T T T

SEQ. ID. NO. 38 C A G A A A A T C C C A C G T G A A C C A A G A C
 SEQ. ID. NO. 34 G A G G G T G T G G T G C G A G C C C T G C T G C
 SEQ. ID. NO. 30 G A G A T C C A G C A T G T G G T A G A G G T G A
 SEQ. ID. NO. 26 G A G G G T G T G G T G C G A G C C C T G C T G C

SEQ. ID. NO. 38 C T G G A G A A T T T G A A A A A T T A T C A A
 SEQ. ID. NO. 34 A G A A G C C C A G T G C C C G C G T G G C T G T
 SEQ. ID. NO. 30 T T C A A A A T T C C A C G G C C A A A G T C A T
 SEQ. ID. NO. 26 A G A A G C C C A G T G C C C G C G T G G C T G T

Figure 9d

SEQ. ID. NO. 38 A C G C C T G C T A G A A A C A C C T A A T G C T
 SEQ. ID. NO. 34 C C T G T T C A C C C G T T C T G A G G A T G C C
 SEQ. ID. NO. 30 C G T G G T T T T C T C C A G T G G C C C A G A T
 SEQ. ID. NO. 26 C C T G T T C A C C C G T T C T G A G G A T G C C

SEQ. ID. NO. 38 C G A G C A G T G A T T A T G T T T G C C A A T G
 SEQ. ID. NO. 34 C G G G A G C T G C T T G C T G C C A G C C A G C
 SEQ. ID. NO. 30 C T T G A G C C C C T C A T C A A G G A G A T T G
 SEQ. ID. NO. 26 C G G G A G C T G C T T G C T G C C A G C C A G C

SEQ. ID. NO. 38 A G G A T G A C A T C A G G A G G A T A T T G G A
 SEQ. ID. NO. 34 G C C T C A A T G C C A G C T T C A C C T G G G T
 SEQ. ID. NO. 30 T C C G G C G C A A T A T C A C G G G C A A G A T
 SEQ. ID. NO. 26 G C C T C A A T G C C A G C T T C A C C T G G G T

SEQ. ID. NO. 38 A G C A G C A A A A A A C T A A A C C A A A G T
 SEQ. ID. NO. 34 G G C C A G T G A T G G T T G G G G G G C C C T G
 SEQ. ID. NO. 30 C T G G C T G G C C A G C G A G G C C T G G G C C
 SEQ. ID. NO. 26 G G C C A G T G A T G G T T G G G G G G C C C T G

SEQ. ID. NO. 38 G G G C A T T T T C T C T G G A T T G G C T C A G
 SEQ. ID. NO. 34 G A G A G T G T G G T G G C A G G C A G T G A G G
 SEQ. ID. NO. 30 A G C T C C T C C C T G A T C G C C A T G C C T C
 SEQ. ID. NO. 26 G A G A G T G T G G T G G C A G G C A G T G A G G

SEQ. ID. NO. 38 A T A G T T G G G G A T C C A A A A T A G C A C C
 SEQ. ID. NO. 34 G G G C T G C T G A G G G T G C T A T C A C C A T
 SEQ. ID. NO. 30 A G T A C T T C C A C G T G G T T G G C G G C A C
 SEQ. ID. NO. 26 G G G C T G C T G A G G G T G C T A T C A C C A T

SEQ. ID. NO. 38 T G T C T A T C A G C A A G A G G A G A T T G C A
 SEQ. ID. NO. 34 C G A G C T G G C C T C C T A C C C C A T C A G T
 SEQ. ID. NO. 30 C A T T G G A T T C G C T C T G A A G G C T G G G
 SEQ. ID. NO. 26 C G A G C T G G C C T C C T A C C C C A T C A G T

SEQ. ID. NO. 38 G A A G G G G C T G T G A C A A T T T T G C C C A
 SEQ. ID. NO. 34 G A C T T T G C C T C C T A C T T C C A G A G C C
 SEQ. ID. NO. 30 C A G A T C C C A G G C T T C C G G G A A T T C C
 SEQ. ID. NO. 26 G A C T T T G C C T C C T A C T T C C A G A G C C

Figure 9e

SEQ. ID. NO. 38 A A C G A G C A T C A A T T G A T G G A T T T G A
 SEQ. ID. NO. 34 T G G A C C C T T G G A A C A A C A G C C G G A A
 SEQ. ID. NO. 30 T G A A G A A G G T C C A T C C C A G G A A G T C
 SEQ. ID. NO. 26 T G G A C C C T T G G A A C A A C A G C C G G A A

SEQ. ID. NO. 38 T C G A T A C T T T A G A A G C C G A A C T C T T
 SEQ. ID. NO. 34 C C C C T G G T T C C G T G A A T T C T G G G A G
 SEQ. ID. NO. 30 T G T C C A C A A T G G T T T T G C C A A G G A G
 SEQ. ID. NO. 26 C C C C T G G T T C C G T G A A T T C T G G G A G

SEQ. ID. NO. 38 G C C A A T A A T C G A A G A A A T G T G T G G T
 SEQ. ID. NO. 34 C A G A G G T T C C G C T G C A G C T T C C G G C
 SEQ. ID. NO. 30 T T T T G G G A A G A A A C A T T T A A C T G C C
 SEQ. ID. NO. 26 C A G A G G T T C C G C T G C A G C T T C C G G C

SEQ. ID. NO. 38 T T G C A G A A T T C T G G G A G G A G A A T T T
 SEQ. ID. NO. 34 A G C G A G A C T G C G C A G C C C A C T C T C T
 SEQ. ID. NO. 30 A C C T C C A A G A A G G T G C A A A A G G A C C
 SEQ. ID. NO. 26 A G C G A G A C T G C G C A G C C C A C T C T C T

SEQ. ID. NO. 38 T G G C T G C A A G T T A G G A T C A C A T G G G
 SEQ. ID. NO. 34 C C G G G C T G T G C C C T T T G A G C A G G A G
 SEQ. ID. NO. 30 T T T A C C T G T G G A C A C C T T T C T G A G A
 SEQ. ID. NO. 26 C C G G G C T G T G C C C T T T G A A C A G G A G

SEQ. ID. NO. 38 A A A A G G A A C A G T C A T A T A A A G A A A T
 SEQ. ID. NO. 34 T C C A A G A T C A T G T T T G T G G T C A A T G
 SEQ. ID. NO. 30 G G T C A C G A A G A A A G T G G C G A C A G G T
 SEQ. ID. NO. 26 T C C A A G A T C A T G T T T G T G G T C A A T G

SEQ. ID. NO. 38 G C A C A G G G C T G G A G C G A A T T G C T C G
 SEQ. ID. NO. 34 C A G T G T A C G C C A T G G C C C A T G C G C T
 SEQ. ID. NO. 30 T T A G C A A C A G C T C G A C A G C C T T C C G
 SEQ. ID. NO. 26 C A G T G T A C G C C A T G G C C C A T G C G C T

SEQ. ID. NO. 38 G G A T T C A T C T T A T G A A C A G G A A G G A
 SEQ. ID. NO. 34 C C A C A A C A T G C A C C G T G C C C T C T G C
 SEQ. ID. NO. 30 A C C C C T C T G T A C A G G G G A T G A G A A C
 SEQ. ID. NO. 26 C C A C A A C A T G C A C C G T G C C C T C T G C

Figure 9f

SEQ. ID. NO. 38 A A G G T C C A A T T T G T A A T T G A T G C T G
 SEQ. ID. NO. 34 C C C A A C A C C A C C C G G C T C T G T G A C G
 SEQ. ID. NO. 30 A T C A G C A G T G T C G A G A C C C C T T A C A
 SEQ. ID. NO. 26 C C C A A C A C C A C C C G G C T C T G T G A C G

SEQ. ID. NO. 38 T A T A T T C C A T G G C T T A C G C C C T G C A
 SEQ. ID. NO. 34 C G A T G C G G C C A G T T A A C G G G C G C C G
 SEQ. ID. NO. 30 T A G A T T A C A C G C A T T T A C G G A T A T C
 SEQ. ID. NO. 26 C G A T G C G G C C A G T T A A C G G G C G C C G

SEQ. ID. NO. 38 C A A T A T G C A C A A A G A T C T C T G C C C T
 SEQ. ID. NO. 34 C C T C T A C A A G G A C T T T G T G C T C A A C
 SEQ. ID. NO. 30 C T A C A A T G T G T A C T T A G C A G T C T A C
 SEQ. ID. NO. 26 C C T C T A C A A G G A C T T T G T G C T C A A C

SEQ. ID. NO. 38 G G A T A C A T T G G C C T T T G T C C A C G A A
 SEQ. ID. NO. 34 G T C A A G T T T G A T G C C C C C T T T C G C C
 SEQ. ID. NO. 30 T C C A T T G C C C A C G C C T T G C A A G A T A
 SEQ. ID. NO. 26 G T C A A G T T T G A T G C C C C C T T T C G C C

SEQ. ID. NO. 38 T G A G T A C C A T T G A T G G G A A A G A G C T
 SEQ. ID. NO. 34 C A G C T G A C A C C C A C A A T G A G G T C C G
 SEQ. ID. NO. 30 T A T A T A C C T G C T T A C C T G G G A G A G G
 SEQ. ID. NO. 26 C A G C T G A C A C C C A C A A T G A G G T C C G

SEQ. ID. NO. 38 A C T T G G T T A T A T T C G G G C T G T A A A T
 SEQ. ID. NO. 34 C T T T G A C C G C T T T G G T G A T G G T A T T
 SEQ. ID. NO. 30 G C T C T T C A C C A A T G G C T C C T G T G C A
 SEQ. ID. NO. 26 C T T T G A C C G C T T T G G T G A T G G T A T T

SEQ. ID. NO. 38 T T T A A T G G C A G T G C T G G C A C T C C T G
 SEQ. ID. NO. 34 G G C C G C T A C A A C A T C T T C A C C T A T C
 SEQ. ID. NO. 30 G A C A T C A A G A A A G T T G A G G C G T G G C
 SEQ. ID. NO. 26 G G C C G C T A C A A C A T C T T C A C C T A T C

SEQ. ID. NO. 38 T C A C T T T T A A T G A A A A C G G A G A T G C
 SEQ. ID. NO. 34 T G C G T G C A G G C A G T G G G C G C T A T C G
 SEQ. ID. NO. 30 A G G T C C T G A A G C A C C T A C G G C A T C T
 SEQ. ID. NO. 26 T G C G T G C A G G C A G T G G G C G C T A T C G

Figure 9g

SEQ. ID. NO. 38 T C C T G G A C G T T A T G A T A T C T T C C A G
 SEQ. ID. NO. 34 C T A C C A G A A G G T G G G C T A C T G G G C A
 SEQ. ID. NO. 30 A A A C T T T A C A A A C A A T A T G G G G G A G
 SEQ. ID. NO. 26 C T A C C A G A A G G T G G G C T A C T G G G C A

SEQ. ID. NO. 38 T A T C A A A T A A C C A A C A A A A G C A C A G
 SEQ. ID. NO. 34 G A A G G C T T G A C T C T G G A C A C C A G C C
 SEQ. ID. NO. 30 C A G G T G A C C T T T G A T G A G T G T G G T G
 SEQ. ID. NO. 26 G A A G G C T T G A C T C T G G A C A C C A G C C

SEQ. ID. NO. 38 A G T A C A A A G T C A T C G G C C A C T G G A C
 SEQ. ID. NO. 34 T C A T C C C A T G G G C C T C A C C C T C A G C
 SEQ. ID. NO. 30 A C C T G G T G G G G A A C T A T T C C A T C A T
 SEQ. ID. NO. 26 T C A T C C C A T G G G C C T C A C C G T C A G C

SEQ. ID. NO. 38 C A A T C A G C T T C A T C T A A A A G T G G A A
 SEQ. ID. NO. 34 C G G C C C C C T G C C C G C C T C T C G C T G C
 SEQ. ID. NO. 30 C A A C T G G C A C C T C T C C C C A G A G G A T
 SEQ. ID. NO. 26 C G G C C C C C T G G C C G C C T C T C G C T G C

SEQ. ID. NO. 38 G A C A T G C A G T G G G C T C A T A G A G A A C
 SEQ. ID. NO. 34 A G T G A G C C C T G C C T C C A G A A T G A G G
 SEQ. ID. NO. 30 G G C T C C A T C G T G T T T A A G G A A G T C G
 SEQ. ID. NO. 26 A G T G A G C C C T G C C T C C A G A A T G A G G

SEQ. ID. NO. 38 A T A C T C A C C C G G C G T C T G T C T G C A G
 SEQ. ID. NO. 34 T G A A G A G T G T G C A G C C G G G C G A A G T
 SEQ. ID. NO. 30 G G T A T T A C A A C G T C T A T G C C A A G A A
 SEQ. ID. NO. 26 T G A A G A G T G T G C A G C C G G G C G A A G T

SEQ. ID. NO. 38 C C T G C C G T G T A A G C C A G G G G A G A G G
 SEQ. ID. NO. 34 C T G C T G C T G G C T C T G C A T T C C G T G C
 SEQ. ID. NO. 30 G G G A G A A A G A C T C T T C A T C A A C G A G
 SEQ. ID. NO. 26 C T G C T G C T G G C T C T G C A T T C C G T G C

SEQ. ID. NO. 38 A A G A A A A C G G T G A A A G G G G T C C C T T
 SEQ. ID. NO. 34 C A G C C C T A T G A G T A C C G A T T G G A C G
 SEQ. ID. NO. 30 G A G A A A A T C C T G T G G A G T G G G T T C T
 SEQ. ID. NO. 26 C A G C C C T A T G A G T A C C G A T T G G A C G

Figure 9h

SEQ. ID. NO. 38 G C T G C T G G C A C T G T G A A C G C T G T G A
 SEQ. ID. NO. 34 A A T T C A C T T G C G C T G A T T G T G G C C T
 SEQ. ID. NO. 30 C C A G G G A G G T G C C C T T C T C C A A C T G
 SEQ. ID. NO. 26 A A T T C A C T T G C G C T G A T T G T G G C C T

SEQ. ID. NO. 38 A G G T T A C A A C T A C C A G G T G G A T G A G
 SEQ. ID. NO. 34 G G G C T A C T G G C C C A A T G C C A G C C T G
 SEQ. ID. NO. 30 C A G C C G A G A C T G C C T G G C A G G G A C C
 SEQ. ID. NO. 26 G G G C T A C T G G C C C A A T G C C A G C C T G

SEQ. ID. NO. 38 C T G T C C T G T G A A C T T T G C C C T C T G G
 SEQ. ID. NO. 34 A C T G G C T G C T T C G A A C T G C C C C A G G
 SEQ. ID. NO. 30 A G G A A A G G G A T C A T T G A G G G G G A G C
 SEQ. ID. NO. 26 A C T G G C T G C T T C G A A C T G C C C C A G G

SEQ. ID. NO. 38 A T C A G A G A C C C A A C A T G A A C C G C A C
 SEQ. ID. NO. 34 A G T A C A T C C G C T G G G G C G A T G C C T G
 SEQ. ID. NO. 30 C C A C C T G C T G C T T T G A G T G T G T G G A
 SEQ. ID. NO. 26 A G T A C A T C C G C T G G G G C G A T G C C T G

SEQ. ID. NO. 38 A G G C T G C C A G C T T A T C C C C A T C A T C
 SEQ. ID. NO. 34 G G C T G T G G G A C C T G T C A C C A T C G C C
 SEQ. ID. NO. 30 G T G T C C T G A T G G G G A G T A T A G T G A T
 SEQ. ID. NO. 26 G G C T G T G G G A C C T G T C A C C A T C G C C

SEQ. ID. NO. 38 A A A T T G G A G T G G C A T T C T C C C T G G G
 SEQ. ID. NO. 34 T G C C T C G G T G C C C T G G C C A C C C T C T
 SEQ. ID. NO. 30 G A G A C A G A T G C C A G T G C C T G T A A C A
 SEQ. ID. NO. 26 T G C C T C G G T G C C C T G G C C A C C C T G T

SEQ. ID. NO. 38 C T G T G G T G C C T G T G T T T G T T G C A A T
 SEQ. ID. NO. 34 T T G T G C T G G G T G T C T T T G T G C G G C A
 SEQ. ID. NO. 30 A G T G C C C A G A T G A C T T C T G G T C C A A
 SEQ. ID. NO. 26 T T G T G C T G G G T G T C T T T G T G C G G C A

SEQ. ID. NO. 38 A T T G G G A A T C A T C G C C A C C A C C T T T
 SEQ. ID. NO. 34 C A A T G C C A C A C C A G T G G T C A A G G C C
 SEQ. ID. NO. 30 T G A G A A C C A C A C C T C C T G C T T C G A A
 SEQ. ID. NO. 26 C A A T G C C A C A C C A G T G G T C A A G G C C

Figure 9i

SEQ. ID. NO. 38 GTGATCGTGACCTTTGTCCGCTATA
 SEQ. ID. NO. 34 TCAGGTCTGGGAGCTCTGCTACATCC
 SEQ. ID. NO. 30 CTGCCCCAGGAGTACATCCGCTGGG
 SEQ. ID. NO. 26 TCAGGTCTGGGAGCTCTGCTACATCC

SEQ. ID. NO. 38 ATGACACACCTATCTGTGAGGGCTTC
 SEQ. ID. NO. 34 TGCTGGGTGGTGTCTTCCTCTGCTA
 SEQ. ID. NO. 30 GCGATGCCCTGGGCTGTGGGACCTGT
 SEQ. ID. NO. 26 TGCTGGGTGGTGTCTTCCTCTGCTA

SEQ. ID. NO. 38 AGGACGCGAACTTAGTTACGTGCTC
 SEQ. ID. NO. 34 CTGCATGACCTTCATCTTCATTGCC
 SEQ. ID. NO. 30 CACCATCGCCTGCCTCGGTGCCCTG
 SEQ. ID. NO. 26 CTGCATGACCTTCATCTTCATTGCC

SEQ. ID. NO. 38 CTAACGGGGATTTTTCTCTGTTATT
 SEQ. ID. NO. 34 AAGCCATCCACGGCAGTGTGTACCT
 SEQ. ID. NO. 30 GCCACCCTGTTTGTGCTGGGTGTCT
 SEQ. ID. NO. 26 AAGCCATCCACGGCAGTGTGTACCT

SEQ. ID. NO. 38 CAATCACGTTTTTTAATGATTGCAGC
 SEQ. ID. NO. 34 TACGGCGTCTTTGGTTTGGGGCACTGC
 SEQ. ID. NO. 30 TTGTGCGGCAACAATGCCACACCAGT
 SEQ. ID. NO. 26 TACGGCGTCTTTGGTTTGGGGCACTGC

SEQ. ID. NO. 38 ACCAGATACAATCATATGCTCCTTC
 SEQ. ID. NO. 34 CTTCTCTGTCTGCTACTCAGCCCTG
 SEQ. ID. NO. 30 GGTCAAGGCCTCAGGTCTGGGAGCTC
 SEQ. ID. NO. 26 CTTCTCTGTCTGCTACTCAGCCCTG

SEQ. ID. NO. 38 CGACGGGTCTTCTCTAGGACTTGGCA
 SEQ. ID. NO. 34 CTCACCAAGACCAACCAGCATTTGCAC
 SEQ. ID. NO. 30 TGCTACATCCTGCTGGGTGGTGTCT
 SEQ. ID. NO. 26 CTCACCAAGACCAACCAGCATTTGCAC

SEQ. ID. NO. 38 TGTGTTTTCAGCTATGCAGCCCTTCT
 SEQ. ID. NO. 34 GCATCTTTCGGTGGGGCCCCGGGAGGG
 SEQ. ID. NO. 30 TCTCTGTCTACTGCATGACCTTCAT
 SEQ. ID. NO. 26 GCATCTTTCGGTGGGGCCCCGGGAGGG

Figure 9j

SEQ. ID. NO. 38 G A C C A A A A C A A A C C G T A T C C A C C G A
 SEQ. ID. NO. 34 T G C C C A G C G G C C A C G C T T C A T C A G T
 SEQ. ID. NO. 30 C T T C A T T G C C A A G C C A T C C A C G G C A
 SEQ. ID. NO. 26 T G C C C A G C G G C C A C G C T T C A T C A G T

SEQ. ID. NO. 38 A T A T T T G A G C A G G G G A A G A A A T C T G
 SEQ. ID. NO. 34 C C T G C C T C A C A G G T G G C C A T C T G C C
 SEQ. ID. NO. 30 G T G T G T A C C T T A C G G C G T C T T G G T T
 SEQ. ID. NO. 26 C C T G C C T C A C A G G T G G C C A T C T G C C

SEQ. ID. NO. 38 T C A C A G C G C C C A A G T T C A T T A G T C C
 SEQ. ID. NO. 34 T G G C A C T T A T C T C G G G C C A G C T G C T
 SEQ. ID. NO. 30 T G G G C A C T G C C T T C T C T G T C T G C T A
 SEQ. ID. NO. 26 T G G C A C T T A T C T C G G G C C A G C T G C T

SEQ. ID. NO. 38 A G C A T C T C A G C T G G T G A T C A C C T T C
 SEQ. ID. NO. 34 C A T C G T G G T C G C C T G G C T G G T G G T G
 SEQ. ID. NO. 30 C T C A G C C C T G C T C A C C A A G A C C A A C
 SEQ. ID. NO. 26 C A T C G T G G T C G C C T G G C T G G T G G T G

SEQ. ID. NO. 38 A G C C T C A T C T C C G T C C A G C T C C T T G
 SEQ. ID. NO. 34 G A G G C A C C G G G C A C A G G C A A G G A G A
 SEQ. ID. NO. 30 C G C A T T G C A C G C A T C T T C G G T G G G G
 SEQ. ID. NO. 26 G A G G C A C C G G G C A C A G G C A A G G A G A

SEQ. ID. NO. 38 G A G T G T T T G T C T G G T T T G T T G T G G A
 SEQ. ID. NO. 34 C A G C C C C C G A A C G G C G G G A G G T G G T
 SEQ. ID. NO. 30 C C C G G G A G G G T G C C C A G C G G C C A C G
 SEQ. ID. NO. 26 C A G C C C C C G A A C G G C G G G A G G T G G T

SEQ. ID. NO. 38 T C C C C C C C A C A T C A T C A T T G A C T A T
 SEQ. ID. NO. 34 G A C A C T G C G C T G C A A C C A C C G C G A T
 SEQ. ID. NO. 30 C T T C A T C A G T C C T G C C T C A C A G G T G
 SEQ. ID. NO. 26 G A C A C T G C G C T G C A A C C A C C G C G A T

SEQ. ID. NO. 38 G G A G A G C A G C G G A C A C T A G A T C C A G
 SEQ. ID. NO. 34 G C A A G T A T G T T G G G C T C G C T G G C C T
 SEQ. ID. NO. 30 G C C A T C T G C C T G G G C A C T T A T C T C G G
 SEQ. ID. NO. 26 G C A A G T A T G T T G G G C T C G C T G G C C T

Figure 9k

SEQ. ID. NO. 38 A G A A G G C C A G G G G A G T G C T C A A G T G
 SEQ. ID. NO. 34 A C A A T G T G C T C C T C A T C G C G C T C T G
 SEQ. ID. NO. 30 G C C A G C T G C T C A T C G T G G T C G C C T G
 SEQ. ID. NO. 26 A C A A T G T G C T C C T C A T C G C G C T C T G

SEQ. ID. NO. 38 T G A C A T T T C T G A T C T C T C A C T C A T T
 SEQ. ID. NO. 34 C A C G C T T T A T G C C T T C A A G A C T C G C
 SEQ. ID. NO. 30 G C T G G T G G T G G A G G C A C C G G G C A C A
 SEQ. ID. NO. 26 C A C G C T T T A T G C C T T C A A T A C T C G C

SEQ. ID. NO. 38 T G T T C A C T T G G A T A C A G T A T C C T C T
 SEQ. ID. NO. 34 A A G T G C C C C G A A A A C T T C A A C G A G G
 SEQ. ID. NO. 30 G G C A A G G A G A C A G C C C C C G A A C G G C
 SEQ. ID. NO. 26 A A G T G C C C C G A A A A C T T C A A C G A G G

SEQ. ID. NO. 38 T G A T G G T C A C T T G T A C T G T T T A T G C
 SEQ. ID. NO. 34 C C A A G T T C A T T G G C T T C A C C A T G T A
 SEQ. ID. NO. 30 G G G A G G T G G T G A C A C T G C G C T G C A A
 SEQ. ID. NO. 26 C C A A G T T C A T T G G C T T C A C C A T G T A

SEQ. ID. NO. 38 C A T T A A A A C G A G A G G T G T C C C A G A G
 SEQ. ID. NO. 34 C A C C A C C T G C A T C A T C T G G C T G G C A
 SEQ. ID. NO. 30 C C A C C G C G A T G C A A G T A T G T T G G G C
 SEQ. ID. NO. 26 C A C C A C C T G C A T C A T C T G G C T G G C A

SEQ. ID. NO. 38 A C T T T C A A T G A A G C C A A A C C T A T T G
 SEQ. ID. NO. 34 T T C C T G C C C A T C T T C T A T G T C A C C T
 SEQ. ID. NO. 30 T C G C T G G C C T A C A A T G T G C T C C T C A
 SEQ. ID. NO. 26 T T G T T G C C C A T C T T C T A T G T C A C C T

SEQ. ID. NO. 38 G A T T T A C C A T G T A T A C C A C C T G C A T
 SEQ. ID. NO. 34 C C A G T G A C T A C C G G G T A C A G A C C A C
 SEQ. ID. NO. 30 T C G C G C T C T G C A C G C T T T A T G C C T T
 SEQ. ID. NO. 26 C C A G T G A C T A C C G G G T A C A G A C C A C

SEQ. ID. NO. 38 C A T T T G G T T A G C T T T C A T C C C C A T C
 SEQ. ID. NO. 34 C A C C A T G T G C G T G T C A G T C A G C C T C
 SEQ. ID. NO. 30 C A A T A C T C G C A A G T G C C C C G A A A A C
 SEQ. ID. NO. 26 C A C C A T G T G C G T G T C A G T C A G C C T C

Figure 91

SEQ. ID. NO. 38 T T T T T T G G T A C A G C C C A G T C A G C A G
 SEQ. ID. NO. 34 A G C G G C T C C G T G G T G C T T G G C T G C C
 SEQ. ID. NO. 30 T T C A A C G A G G C C A A G T T C A T T G G C T
 SEQ. ID. NO. 26 A G C G G C T C C G T G G T G C T T G G C T G C C

SEQ. ID. NO. 38 A A A A G A T G T A C A T C C A G A C A A C A A C
 SEQ. ID. NO. 34 T C T T T G C G C C C A A G C T G C A C A T C A T
 SEQ. ID. NO. 30 T C A C C A T G T A C A C C A C C T G C A T C A T
 SEQ. ID. NO. 26 T C T T T G C G C C C A A G C T G C A C A T C A T

SEQ. ID. NO. 38 A C T T A C T G T C T C C A T G A G T T T A A G T
 SEQ. ID. NO. 34 C C T C T T C C A G C C G C A G A A G A A C A C C
 SEQ. ID. NO. 30 C T G G C T G G C A T T G T T G C C C A T C T T C
 SEQ. ID. NO. 26 C C T C T T C C A G C C G C A G A A G A A C G T G

SEQ. ID. NO. 38 G C T T C A G T A T C T C T G G G C A T G C T C T
 SEQ. ID. NO. 34 A T C G A G G A G G T G C G T T G C A G C A C C G
 SEQ. ID. NO. 30 T A T G T C A C C T C C A G T G A C T A C C G G G
 SEQ. ID. NO. 26 G T T A G C C A C C G G G C A C C C A C C A G C C

SEQ. ID. NO. 38 A T A T G C C C A A G G T T T A T A T T A T A A T
 SEQ. ID. NO. 34 C A G C T C A C G C T T T C A A G G T G G C T G C
 SEQ. ID. NO. 30 T A C A G A C C A C C A C C A T G T G C G T G T C
 SEQ. ID. NO. 26 G C T T T G G C A G T G C T G C T G C C A G G G C

SEQ. ID. NO. 38 T T T T C A T C C A G A A C A G A A T A C C A T C
 SEQ. ID. NO. 34 C C G G G C C A C G C T G C G C C G C A G C A A C
 SEQ. ID. NO. 30 A G T C A G C C T C A G C G G C T C C G T G G T G
 SEQ. ID. NO. 26 C A G C T C C A G C C T T G G C C A A G G G T C T

SEQ. ID. NO. 38 G A G G A G G T G C G T T G C A G C A C C G C A G
 SEQ. ID. NO. 34 G T C T C C C G C A A G C G G T C C A G C A G C C
 SEQ. ID. NO. 30 C T T G G C T G C C T C T T T G C G C C C A A G C
 SEQ. ID. NO. 26 G G C T C C C A G T T T G T C C C C A C T G T T T

SEQ. ID. NO. 38 C T C A C G C T T T C A A G G T G G C T G C C C G
 SEQ. ID. NO. 34 T T G G A G G C T C C A C G G G A T C C A C C C C
 SEQ. ID. NO. 30 T G C A C A T C A T C C T C T T C C A G C C G C A
 SEQ. ID. NO. 26 G C A A T G G C C G T G A G G T G G T G G A C T C

Figure 9m

SEQ. ID. NO. 38 G G C C A C G C T G C G C C G C A G C A A C G T C
 SEQ. ID. NO. 34 C T C C T C C T C C A T C A G C A G C A A G A G C
 SEQ. ID. NO. 30 G A A G A A C G T G G T T A G C C A C C G G G C A
 SEQ. ID. NO. 26 G A C A A C G T C A T C G C T T

SEQ. ID. NO. 38 T C C C G C A A G C G G T C C A G C A G C C T T G
 SEQ. ID. NO. 34 A A C A G C G A A G A C C C A T T C C C A C A G C
 SEQ. ID. NO. 30 C C C A C C A G C C G C T T T G G C A G T G C T G
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G A G G C T C C A C G G G A T C C A C C C C C T C
 SEQ. ID. NO. 34 C C G A G A G G C A G A A G C A G C A G C A G C C
 SEQ. ID. NO. 30 C T G C C A G G G C C A G C T C C A G C C T T G G
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 C T C C T C C A T C A G C A G C A A G A G C A A C
 SEQ. ID. NO. 34 G C T G G C C C T A A C C C A G C A A G A G C A G
 SEQ. ID. NO. 30 C C A A G G G T C T G G C T C C C A G T T T G T C
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G C G A A G A C C C A T T C C C A C A G C C C G
 SEQ. ID. NO. 34 C A G C A G C A G C C C C T G A C C C T C C C A C
 SEQ. ID. NO. 30 C C C A C T G T T T G C A A T G G C C G T G A G G
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G A G G C A G A A G C A G C A G C A G C C G C T
 SEQ. ID. NO. 34 A G C A G C A A C G A T C T C A G C A G C A G C C
 SEQ. ID. NO. 30 T G G T G G A C T C G A C A A C G T C A T C G C T
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G G C C C T A A C C C A G C A A G A G C A G C A G
 SEQ. ID. NO. 34 C A G A T G C A A G C A G A A G G T C A T C T T T
 SEQ. ID. NO. 30 T
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A G C A G C C C C T G A C C C T C C C A C A G C
 SEQ. ID. NO. 34 G G C A G C G G C A C G G T C A C C T T C T C A C
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

Figure 9n

SEQ. ID. NO. 38 A G C A A C G A T C T C A G C A G C A G C C C A G
 SEQ. ID. NO. 34 T G A G C T T T G A T G A G C C T C A G A A G A A
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 A T G C A A G C A G A A G G T C A T C T T T G G C
 SEQ. ID. NO. 34 C G C C A T G G C C C A C G G G A A T T C T A C G
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G C G G C A C G G T C A C C T T C T C A C T G A
 SEQ. ID. NO. 34 C A C C A G A A C T C C C T G G A G G C C C A G A
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C T T T G A T G A G C C T C A G A A G A A C G C
 SEQ. ID. NO. 34 A A A G C A G C G A T A C G C T G A C C C G A C A
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A T G G C C C A C G G G A A T T C T A C G C A C
 SEQ. ID. NO. 34 C C A G C C A T T A C T C C C G C T G C A G T G C
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A G A A C T C C C T G G A G G C C C A G A A A A
 SEQ. ID. NO. 34 G G G G A A A C G G A C T T A G A T C T G A C C G
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C A G C G A T A C G C T G A C C C G A C A C C A
 SEQ. ID. NO. 34 T C C A G G A A A C A G G T C T G C A A G G A C C
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C C A T T A C T C C C G C T G C A G T G C G G G
 SEQ. ID. NO. 34 T G T G G G T G G A G A C C A G C G G C C A G A G
 SEQ. ID. NO. 30
 SEQ. ID. NO. 26

Figure 9o

SEQ. ID. NO. 38 G A A A C G G A C T T A G A T C T G A C C G T C C
SEQ. ID. NO. 34 G T G G A G G A C C C T G A A G A G T T G T C C C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G G A A A C A G G T C T G C A A G G A C C T G T
SEQ. ID. NO. 34 C A G C A C T T G T A G T G T C C A G T T C A C A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G G G T G G A G A C C A G C G G C C A G A G G T G
SEQ. ID. NO. 34 G A G C T T T G T C A T C A G T G G T G G A G G C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G A G G A C C C T G A A G A G T T G T C C C C A G
SEQ. ID. NO. 34 A G C A C T G T T A C A G A A A C G T A G T G A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A C T T G T A G T G T C C A G T T C A C A G A G
SEQ. ID. NO. 34 A T T C A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C T T T G T C A T C A G T G G T G G A G G C A G C
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A C T G T T A C A G A A A C G T A G T G A A T T
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

Figure 9p

ClustalW Formatted Alignments

SEQ. ID. NO. 39 M V C E G K R S A S C P C F F L L T A K F Y W I L
 SEQ. ID. NO. 35 M G S L L A L P A L L L L W G A V A E G P A K K V
 SEQ. ID. NO. 31 M A F Y S C C W V L L A L T W H T S A Y G P D Q R
 SEQ. ID. NO. 27 M G S L L A L L A L L P L W G A V A E G P A K K V

SEQ. ID. NO. 39 T M M Q R T H S Q E Y A H S I R V D G D I I L G G
 SEQ. ID. NO. 35 L T L E G D L V L G G L F P V H Q K G G P A E D C
 SEQ. ID. NO. 31 A Q K K G D I I L G G L F P I H F G V A A K D Q D
 SEQ. ID. NO. 27 L T L E G D L V L G G L F P V H Q K G G P A E D C

SEQ. ID. NO. 39 L F P V H A K G E R G V P C G E L K K E K G I H R
 SEQ. ID. NO. 35 G P V N E H R G I Q R L E A M L F A L D R I N R D
 SEQ. ID. NO. 31 L K S R P E S V E C I R Y N F R G F R W L Q A M I
 SEQ. ID. NO. 27 G P V N E H R G I Q R L E A M L F A L D R I N R D

SEQ. ID. NO. 39 L E A M L Y A I D Q I N K D P D L L S N I T L G V
 SEQ. ID. NO. 35 P H L L P G V R L G A H I L D S C S K D T H A L E
 SEQ. ID. NO. 31 F A I E E I N S S P A L L P N L T L G Y R I F D T
 SEQ. ID. NO. 27 P H L L P G V R L G A H I L D S C S K D T H A L E

SEQ. ID. NO. 39 R I L D T C S R D T Y A L E Q S L T F V Q A L I E
 SEQ. ID. NO. 35 Q A L D F V R A S L S R G A D G S R H I C P D G S
 SEQ. ID. NO. 31 C N T V S K A L E A T L S F V A Q N K I D S L N L
 SEQ. ID. NO. 27 Q A L D F V R A S L S R G A D G S R H I C P D G S

SEQ. ID. NO. 39 K D A S D V K C A N G D P P I F T K P D K I S G V
 SEQ. ID. NO. 35 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
 SEQ. ID. NO. 31 D E F C N C S E H I P S T I A V V G A T G S G V S
 SEQ. ID. NO. 27 Y A T H G D A P T A I T G V I G G S Y S D V S I Q

SEQ. ID. NO. 39 I G A A A S S V S I M V A N I L R L F K I P Q I S
 SEQ. ID. NO. 35 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
 SEQ. ID. NO. 31 T A V A N L L G L F Y I P Q V S Y A S S S R L L S
 SEQ. ID. NO. 27 V A N L L R L F Q I P Q I S Y A S T S A K L S D K

SEQ. ID. NO. 39 Y A S T A P E L S D N T R Y D F F S R V V P P D S
 SEQ. ID. NO. 35 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
 SEQ. ID. NO. 31 N K N Q F K S F L R T I P N D E H Q A T A M A D I
 SEQ. ID. NO. 27 S R Y D Y F A R T V P P D F F Q A K A M A E I L R

Figure 10a

SEQ. ID. NO. 39 YQAQAMVDIVTALGWNYVSTLASEG
 SEQ. ID. NO. 35 FFNWTVYSTVASEGDYGETGIEAFE
 SEQ. ID. NO. 31 IEYFRWNWVGTTAAADDDYGRPGIEK
 SEQ. ID. NO. 27 FFNWTVYSTEASEGDYGETGIEAFE

SEQ. ID. NO. 39 NYGESGVEAFTQISREIGGVCI AQ S
 SEQ. ID. NO. 35 LEARARNICVATSEKVGGRAMSRAAF
 SEQ. ID. NO. 31 FREEAEERDIDIDFSELISQYSDEE
 SEQ. ID. NO. 27 LEARARNICVATSEKVGGRAMSRAAF

SEQ. ID. NO. 39 QKIPREPRPGEFEKI IKRLLLETPNA
 SEQ. ID. NO. 35 EGVVRALLQKPSARVAVLFTRSEDA
 SEQ. ID. NO. 31 EIQHVVEVIQNSTAKVIVVFSSGPD
 SEQ. ID. NO. 27 EGVVRALLQKPSARVAVLFTRSEDA

SEQ. ID. NO. 39 RAVIMFANEDDIRRILEAAKKLNQS
 SEQ. ID. NO. 35 REL LAASQRLNASFTWVASD GWGAL
 SEQ. ID. NO. 31 LEPLIKEIVRRNITGKIWLASEAWA
 SEQ. ID. NO. 27 REL LAASQRLNASFTWVASD GWGAL

SEQ. ID. NO. 39 GHFLWIGSDSWGSKIAPVYQQEEIA
 SEQ. ID. NO. 35 ESVVAGSEGA AEGAITIELASYPIS
 SEQ. ID. NO. 31 SSSLIAMPQYFHVVG GTIGFALKAG
 SEQ. ID. NO. 27 ESVVAGSEGA AEGAITIELASYPIS

SEQ. ID. NO. 39 EGAVTILPKRASIDGFDRYFRSRTL
 SEQ. ID. NO. 35 DFASYFQSLDPWNNNSRNPWFREFWE
 SEQ. ID. NO. 31 QIPGFREFLKKVHPRKSVHNGFAKE
 SEQ. ID. NO. 27 DFASYFQSLDPWNNNSRNPWFREFWE

SEQ. ID. NO. 39 ANNRRNVWF AEFW EENFGCKLGSHG
 SEQ. ID. NO. 35 QRFRC SFRQRDCAAHSLRAVPFEQE
 SEQ. ID. NO. 31 FWEETFNCHLQEGAKGPLPVD TFLR
 SEQ. ID. NO. 27 QRFRC SFRQRDCAAHSLRAVPFEQE

SEQ. ID. NO. 39 KRN SHIKKCTGLER IARDSSSYEQEG
 SEQ. ID. NO. 35 SKIMFVVNAVYAMAHALHNMHRA LC
 SEQ. ID. NO. 31 GHEESGDRFSNSSTA FRPLCTGDEN
 SEQ. ID. NO. 27 SKIMFVVNAVYAMAHALHNMHRA LC

Figure 10b

SEQ. ID. NO. 39 K V Q F V I D A V Y S M A Y A L H N M H K D L C P
 SEQ. ID. NO. 35 P N T T R L C D A M R P V N G R R L Y K D F V L N
 SEQ. ID. NO. 31 I S S V B T P Y I D Y T H L R I S Y N V Y L A V Y
 SEQ. ID. NO. 27 P N T T R L C D A M R P V N G R R L Y K D F V L N

SEQ. ID. NO. 39 G Y I G L C P R M S T I D G K E L L G Y I R A V N
 SEQ. ID. NO. 35 V K F D A P F R P A D T H N E V R F D R F G D G I
 SEQ. ID. NO. 31 S I A H A L Q D I Y T C L P G R G L F T N G S C A
 SEQ. ID. NO. 27 V K F D A P F R P A D T H N E V R F D R F G D G I

SEQ. ID. NO. 39 F N G S A G T P V T F N E N G D A P G R Y D I F Q
 SEQ. ID. NO. 35 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
 SEQ. ID. NO. 31 D I K K V E A W Q V L K H L R H L N F T N N M G E
 SEQ. ID. NO. 27 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A

SEQ. ID. NO. 39 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E
 SEQ. ID. NO. 35 E G L T L D T S L I P W A S P S A G P L P A S R C
 SEQ. ID. NO. 31 Q V T F D E C G D L V G N Y S I I N W H L S P E D
 SEQ. ID. NO. 27 E G L T L D T S L I P W A S P S A G P L A A S R C

SEQ. ID. NO. 39 D M Q W A H R E H T H P A S V C S L P C K P G E R
 SEQ. ID. NO. 35 S E P C L Q N E V K S V Q P G E V C C W L C I P C
 SEQ. ID. NO. 31 G S I V F K E V G Y Y N V Y A K K G E R L F I N E
 SEQ. ID. NO. 27 S E P C L Q N E V K S V Q P G E V C C W L C I P C

SEQ. ID. NO. 39 K K T V K G V P C C W H C E R C E G Y N Y Q V D E
 SEQ. ID. NO. 35 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
 SEQ. ID. NO. 31 E K I L W S G F S R E V P F S N C S R D C L A G T
 SEQ. ID. NO. 27 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L

SEQ. ID. NO. 39 L S C E L C P L D Q R P N M N R T G C Q L I P I I
 SEQ. ID. NO. 35 T G C F E L P Q E Y I R W G D A W A V G P V T I A
 SEQ. ID. NO. 31 R K G I I E G E P T C C F E C V E C P D G E Y S D
 SEQ. ID. NO. 27 T G C F E L P Q E Y I R W G D A W A V G P V T I A

SEQ. ID. NO. 39 K L E W H S P W A V V P V F V A I L G I I A T T F
 SEQ. ID. NO. 35 C L G A L A T L F V L G V F V R H N A T P V V K A
 SEQ. ID. NO. 31 B T D A S A C N K C P D D F W S N E N H T S C F E
 SEQ. ID. NO. 27 C L G A L A T L F V L G V F V R H N A T P V V K A

Figure 10c

SEQ. ID. NO. 39 V I V T F V R Y N D T P I V R A S G R E L S Y V L
 SEQ. ID. NO. 35 S G R E L C Y I L L G G V F L C Y C M T F I F I A
 SEQ. ID. NO. 31 L P Q E Y I R W G D A W A V G P V T I A C L G A L
 SEQ. ID. NO. 27 S G R E L C Y I L L G G V F L C Y C M T F I F I A

SEQ. ID. NO. 39 L T G I F L C Y S I T F L M I A A P D T I I C S F
 SEQ. ID. NO. 35 K P S T A V C T L R R L G L G T A F S V C Y S A L
 SEQ. ID. NO. 31 A T L F V L G V F V R H N A T P V V K A S G R E L
 SEQ. ID. NO. 27 K P S T A V C T L R R L G L G T A F S V C Y S A L

SEQ. ID. NO. 39 R R V F L G L G M C F S Y A A L L T K T N R I H R
 SEQ. ID. NO. 35 L T K T N R I A R I F G G A R E G A Q R P R F I S
 SEQ. ID. NO. 31 C Y I L L G G V F L C Y C M T F I F I A K P S T A
 SEQ. ID. NO. 27 L T K T N R I A R I F G G A R E G A Q R P R F I S

SEQ. ID. NO. 39 I F E Q G K K S V T A P K F I S P A S Q L V I T F
 SEQ. ID. NO. 35 P A S Q V A I C L A L I S G Q L L I V V A W L V V
 SEQ. ID. NO. 31 V C T L R R L G L G T A F S V C Y S A L L T K T N
 SEQ. ID. NO. 27 P A S Q V A I C L A L I S G Q L L I V V A W L V V

SEQ. ID. NO. 39 S L I S V Q L L G V F V W F V V D P P H I I I D Y
 SEQ. ID. NO. 35 E A P G T G K E T A P E R R E V V T L R C N H R D
 SEQ. ID. NO. 31 R I A R I F G G A R E G A Q R P R F I S P A S Q V
 SEQ. ID. NO. 27 E A P G T G K E T A P E R R E V V T L R C N H R D

SEQ. ID. NO. 39 G E Q R T L D P E K A R G V L K C D I S D L S L I
 SEQ. ID. NO. 35 A S M L G S L A Y N V L L I A L C T L Y A F K T R
 SEQ. ID. NO. 31 A I C L A L I S G Q L L I V V A W L V V E A P G T
 SEQ. ID. NO. 27 A S M L G S L A Y N V L L I A L C T L Y A F N T R

SEQ. ID. NO. 39 C S L G Y S I L L M V T C T V Y A I K T R G V P E
 SEQ. ID. NO. 35 K C P E N F N E A K F I G F T M Y T T C I I W L A
 SEQ. ID. NO. 31 G K E T A P E R R E V V T L R C N H R D A S M L G
 SEQ. ID. NO. 27 K C P E N F N E A K F I G F T M Y T T C I I W L A

SEQ. ID. NO. 39 T F N E A K P I G F T M Y T T C I I W L A F I P I
 SEQ. ID. NO. 35 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
 SEQ. ID. NO. 31 S L A Y N V L L I A L C T L Y A F N T R K C P E N
 SEQ. ID. NO. 27 L L P I F Y V T S S D Y R V Q T T T M C V S V S L

Figure 10d

SEQ. ID. NO. 39 P F G T A Q S A E K M Y I Q T T T L T V S M S L S
 SEQ. ID. NO. 35 S G S V V L G C L F A P K L H I I L F Q P Q K N T
 SEQ. ID. NO. 31 F N E A K F I G F T M Y T T C I I W L A L L P I F
 SEQ. ID. NO. 27 S G S V V L G C L F A P K L H I I L F Q P Q K N

SEQ. ID. NO. 39 A S V S L G M L Y M P K V Y I I I F H P E Q N T I
 SEQ. ID. NO. 35 I E E V R C S T A A H A F K V A A R A T L R R S N
 SEQ. ID. NO. 31 Y V T S S D Y R V Q T T T M C V S V S L S G S V V
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 E E V R C S T A A H A F K V A A R A T L R R S N V
 SEQ. ID. NO. 35 V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 31 L G C L F A P K L H I I L F Q P Q K N V V S H R A
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 S R K R S S S L G G S T G S T P S S S I S S K S N
 SEQ. ID. NO. 35 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
 SEQ. ID. NO. 31 P T S R F G S A A R A S S S L G Q G S G S Q F V
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q
 SEQ. ID. NO. 35 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
 SEQ. ID. NO. 31 P T V C N G R E V V D S T T S S L
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F G
 SEQ. ID. NO. 35 G S G T V T F S L S F D E P Q K N A M A H G N S T
 SEQ. ID. NO. 31
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 S G T V T F S L S F D E P Q K N A M A H G N S T H
 SEQ. ID. NO. 35 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
 SEQ. ID. NO. 31
 SEQ. ID. NO. 27

SEQ. ID. NO. 39 Q N S L E A Q K S S D T L T R H Q P L L P L Q C G
 SEQ. ID. NO. 35 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
 SEQ. ID. NO. 31
 SEQ. ID. NO. 27

Figure 10e

SEQ. ID. NO. 39 E T D L D L T V Q E T G L Q G P V G G D Q R P E V
SEQ. ID. NO. 35 V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 31
SEQ. ID. NO. 27

SEQ. ID. NO. 39 E D P E E L S P A L V V S S S Q S F V I S G G G S
SEQ. ID. NO. 35 S T V T E N V V N S
SEQ. ID. NO. 31
SEQ. ID. NO. 27

SEQ. ID. NO. 39 T V T E N V V N S
SEQ. ID. NO. 35
SEQ. ID. NO. 31
SEQ. ID. NO. 27

ClustalW Formatted Alignments

SEQ. ID. NO. 40 A T G G T A T G C G A G G G A A A G C G A T C A G
 SEQ. ID. NO. 46 A T G G G A T C G C T G C T T G C G C T C C C G G
 SEQ. ID. NO. 36 A T G G G A T C G C T G C T T G C G C T C C C G G
 SEQ. ID. NO. 32 A T G G C A T T T T A T A G C T G C T G C T G G G

SEQ. ID. NO. 40 C C T C T T G C C C T T G T T T C T T C C T C T T
 SEQ. ID. NO. 46 C A C T G C T G C T G C T G T G G G G T G C T G T
 SEQ. ID. NO. 36 C A C T G C T G C T G C T G T G G G G T G C T G T
 SEQ. ID. NO. 32 T C C T C T T G G C A C T C A C C T G G C A C A C

SEQ. ID. NO. 40 G A C C G C C A A G T T C T A C T G G A T C C T C
 SEQ. ID. NO. 46 G G C T G A G G G C C C A G C C A A G A A A G G T G
 SEQ. ID. NO. 36 G G C T G A G G G C C C A G C C A A G A A A G G T G
 SEQ. ID. NO. 32 C T C T G C C T A C G G G C C A G A C C A G C G A

SEQ. ID. NO. 40 A C A A T G A T G C A A A G A A A C T C A C A G C C
 SEQ. ID. NO. 46 C T G A C C C T G G A G G G A G A C T T G G T G C
 SEQ. ID. NO. 36 C T G A C C C T G G A G G G A G A C T T G G T G C
 SEQ. ID. NO. 32 G C C C A A A A G A A A G G G G G A C A T T A T C C

SEQ. ID. NO. 40 A G G A G T A T G C C C A T T C C A T A C G G G T
 SEQ. ID. NO. 46 T G G G T G G G C T G T T C C C A G T G C A C C A
 SEQ. ID. NO. 36 T G G G T G G G C T G T T C C C A G T G C A C C A
 SEQ. ID. NO. 32 T T G G G G G G C T C T T T C C T A T T C A T T T

SEQ. ID. NO. 40 G G A T G G G G A C A T T A T T T T G G G G G G T
 SEQ. ID. NO. 46 G A A G G G C G G C C C A G C A G A G G A C T G T
 SEQ. ID. NO. 36 G A A G G G C G G C C C A G C A G A G G A C T G T
 SEQ. ID. NO. 32 T G G A G T A G C A G C T A A A G A T C A A G A T

SEQ. ID. NO. 40 C T C T T C C C T G T C C A C G C A A A G G G A G
 SEQ. ID. NO. 46 G G T C C T G T C A A T G A G C A C C G T G G C A
 SEQ. ID. NO. 36 G G T C C T G T C A A T G A G C A C C G T G G C A
 SEQ. ID. NO. 32 C T C A A A T C A A G G C C G G A G T C T G T G G

SEQ. ID. NO. 40 A G A G A G G G G T G C C T T G T G G G G A G C T
 SEQ. ID. NO. 46 T C C A G C G C C T G G A G G C C A T G C T T T T
 SEQ. ID. NO. 36 T C C A G C G C C T G G A G G C C A T G C T T T T
 SEQ. ID. NO. 32 A A T G T A T C A G G T A T A A T T T C C G T G G

Figure 11a

SEQ. ID. NO. 40 G A A G A A G G A A A A G G G G A T T C A C A G A
 SEQ. ID. NO. 46 T G C A C T G G A C C G C A T C A A C C G T G A C
 SEQ. ID. NO. 36 T G C A C T G G A C C G C A T C A A C C G T G A C
 SEQ. ID. NO. 32 G T T T C G C T G G T T A C A G G C T A T G A T A

SEQ. ID. NO. 40 C T G G A G G C C A T G C T T T A T G C A A T T G
 SEQ. ID. NO. 46 C C G C A C C T G C T G C C T G G C G T G C G C C
 SEQ. ID. NO. 36 C C G C A C C T G C T G C C T G G C G T G C G C C
 SEQ. ID. NO. 32 T T T G C C A T A G A G G A G A T A A A C A G C A

SEQ. ID. NO. 40 A C C A G A T T A A C A A A G G A C C C T G A T C T
 SEQ. ID. NO. 46 T G G G T G C A C A C A T C C T C G A C A G T T G
 SEQ. ID. NO. 36 T G G G T G C A C A C A T C C T C G A C A G T T G
 SEQ. ID. NO. 32 G C C C A G C C C T T C T T C C C A A C T T G A C

SEQ. ID. NO. 40 C C T T T C C A A C A T C A C T C T G G G T G T C
 SEQ. ID. NO. 46 C T C C A A G G A C A C A C A T G C G C T G G A G
 SEQ. ID. NO. 36 C T C C A A G G A C A C A C A T G C G C T G G A G
 SEQ. ID. NO. 32 G C T G G G A T A C A G G A T A T T T G A C A C T

SEQ. ID. NO. 40 C G C A T C C T C G A C A C G T G C T C T A G G G
 SEQ. ID. NO. 46 C A G G C A C T G G A C T T T T G T G C G T G C C T
 SEQ. ID. NO. 36 C A G G C A C T G G A C T T T T G T G C G T G C C T
 SEQ. ID. NO. 32 T G C A A C A C C G T T T C T A A G G C C T T G G

SEQ. ID. NO. 40 A C A C C T A T G C T T T T G G A G C A G T C T C T
 SEQ. ID. NO. 46 C A C T C A G C C G T G G T G C T G A T G G C T C
 SEQ. ID. NO. 36 C A C T C A G C C G T G G T G C T G A T G G C T C
 SEQ. ID. NO. 32 A A G C C A C C C T G A G T T T T G T T G C T C A

SEQ. ID. NO. 40 A A C A T T C G T G C A G G C A T T A A T A G A G
 SEQ. ID. NO. 46 A C G C C A C A T C T G C C C C G A C G G C T C T
 SEQ. ID. NO. 36 A C G C C A C A T C T G C C C C G A C G G C T C T
 SEQ. ID. NO. 32 A A A C A A A A T T G A T T C T T T G A A C C T T

SEQ. ID. NO. 40 A A A G A T G C T T C G G A T G T G A A G T G T G
 SEQ. ID. NO. 46 T A T G C G A C C C A T G G T G A T G C T C C C A
 SEQ. ID. NO. 36 T A T G C G A C C C A T G G T G A T G C T C C C A
 SEQ. ID. NO. 32 G A T G A G T T C T G C A A C T G C T C A G A G C

Figure 11b

SEQ. ID. NO. 40 C T A A T G G A G A T C C A C C C A T T T T C A C
 SEQ. ID. NO. 46 C T G C C A T C A C T G G T G T T A T T G G C G G
 SEQ. ID. NO. 36 C T G C C A T C A C T G G T G T T A T T G G C G G
 SEQ. ID. NO. 32 A C A T T C C C T C T A C G A T T G C T G T G G T

SEQ. ID. NO. 40 C A A G C C C G A C A A G A T T T C T G G C G T C
 SEQ. ID. NO. 46 T T C C T A C A G T G A T G T C T C C A T C C A G
 SEQ. ID. NO. 36 T T C C T A C A G T G A T G T C T C C A T C C A G
 SEQ. ID. NO. 32 G G G A G C A A C T G G C T C A G G C G T C T C C

SEQ. ID. NO. 40 A T A G G T G C T G C A G C A A G C T C C G T G T
 SEQ. ID. NO. 46 G T G G C C A A C C T C T T G A G G C T A T T T C
 SEQ. ID. NO. 36 G T G G C C A A C C T C T T G A G G C T A T T T C
 SEQ. ID. NO. 32 A C G G C A G T G G C A A A T C T G C T G G G G C

SEQ. ID. NO. 40 C C A T C A T G G T T G C T A A C A T T T T A A G
 SEQ. ID. NO. 46 A G A T C C C A C A G A T T A G C T A C G C C T C
 SEQ. ID. NO. 36 A G A T C C C A C A G A T T A G C T A C G C C T C
 SEQ. ID. NO. 32 T C T T C T A C A T T C C C A G G T C A G T T A

SEQ. ID. NO. 40 A C T T T T T A A G A T A C C T C A A A T C A G C
 SEQ. ID. NO. 46 T A C C A G T G C C A A G C T G A G T G A C A A G
 SEQ. ID. NO. 36 T A C C A G T G C C A A G C T G A G T G A C A A G
 SEQ. ID. NO. 32 T G C C T C C T C C A G C A G A C T C C T C A G C

SEQ. ID. NO. 40 T A T G C A T C C A C A G C C C C A G A G C T A A
 SEQ. ID. NO. 46 T C C C G C T A T G A C T A C T T T G C C C G C A
 SEQ. ID. NO. 36 T C C C G C T A T G A C T A C T T T G C C C G C A
 SEQ. ID. NO. 32 A A C A A G A A T C A A T T C A A G T C T T T C C

SEQ. ID. NO. 40 G T G A T A A C A C C A G G T A T G A C T T T T T
 SEQ. ID. NO. 46 C A G T G C C T C C T G A C T T C T T C C A A G C
 SEQ. ID. NO. 36 C A G T G C C T C C T G A C T T C T T C C A A G C
 SEQ. ID. NO. 32 T C C G A A C C A T C C C C A A T G A T G A G C A

SEQ. ID. NO. 40 C T C T C G A G T G G T T C C G C C T G A C T C C
 SEQ. ID. NO. 46 C A A G G C C A T G G C T G A G A T T C T C C G C
 SEQ. ID. NO. 36 C A A G G C C A T G G C T G A G A T T C T C C G C
 SEQ. ID. NO. 32 C C A G G C C A C T G C C A T G G C A G A C A T C

Figure 11c

SEQ. ID. NO. 40 T A C C A A G C C C A A G C C A T G G T G G A C A
 SEQ. ID. NO. 46 T T C T T C A A C T G G A C C T A T G T G T C C A
 SEQ. ID. NO. 36 T T C T T C A A C T G G A C C T A T G T G T C C A
 SEQ. ID. NO. 32 A T C G A G T A T T T T C C G C T G G A A C T G G G

SEQ. ID. NO. 40 T C G T G A C A G C A C T G G G A T G G A A T T A
 SEQ. ID. NO. 46 C T G T G G C G T C T G A G G G C G A C T A T G G
 SEQ. ID. NO. 36 C T G T G G C G T C T G A G G G C G A C T A T G G
 SEQ. ID. NO. 32 T G G G C A C A A T T G C A G C T G A T G A C G A

SEQ. ID. NO. 40 T G T T T C G A C A C T G G C T T C T G A G G G G
 SEQ. ID. NO. 46 C G A G A C A G G C A T T G A G G C C T T T G A G
 SEQ. ID. NO. 36 C G A G A C A G G C A T T G A G G C C T T T G A G
 SEQ. ID. NO. 32 C T A T G G G C G G C C G G G G A T T G A G A A A

SEQ. ID. NO. 40 A A C T A T G G T G A G A G C G G T G T G G A G G
 SEQ. ID. NO. 46 C T A G A G G C T C G T G C C C G C A A C A T C T
 SEQ. ID. NO. 36 C T A G A G G C T C G T G C C C G C A A C A T C T
 SEQ. ID. NO. 32 T T C C G A G A G G A A G C T G A G G A A A G G G

SEQ. ID. NO. 40 C C T T C A C C C A G A T C T C G A G G G A G A T
 SEQ. ID. NO. 46 G T G T G G C C A C C T C G G A G A A A G T G G G
 SEQ. ID. NO. 36 G T G T G G C C A C C T C G G A G A A A G T G G G
 SEQ. ID. NO. 32 A T A T C T G C A T C G A C T T C A G T G A A C T

SEQ. ID. NO. 40 T G G T G G T G T T T G C A T T G C T C A G T C A
 SEQ. ID. NO. 46 C C G T G C C A T G A G C C G C G C G G C C T T T
 SEQ. ID. NO. 36 C C G T G C C A T G A G C C G C G C G G C C T T T
 SEQ. ID. NO. 32 C A T C T C C C A G T A C T C T G A T G A G G A A

SEQ. ID. NO. 40 C A G A A A A T C C C A C G T G A A C C A A G A C
 SEQ. ID. NO. 46 G A G G G T G T G G T G C G A G C C C T G C T G C
 SEQ. ID. NO. 36 G A G G G T G T G G T G C G A G C C C T G C T G C
 SEQ. ID. NO. 32 G A G A T C C A G C A T G T G G T A G A G G T G A

SEQ. ID. NO. 40 C T G G A G A A T T T G A A A A A T T A T C A A
 SEQ. ID. NO. 46 A G A A G C C C A G T G C C C G C G T G G C T G T
 SEQ. ID. NO. 36 A G A A G C C C A G T G C C C G C G T G G C T G T
 SEQ. ID. NO. 32 T T C A A A A T T C C A C G G C C A A A G T C A T

Figure 11d

SEQ. ID. NO. 40 A C G C C T G C T A G A A A C A C C T A A T G C T
 SEQ. ID. NO. 46 C C T G T T C A C C C G T T C T G A G G A T G C C
 SEQ. ID. NO. 36 C C T G T T C A C C C G T T C T G A G G A T G C C
 SEQ. ID. NO. 32 C G T G G T T T T C T C A G T G G C C C A G A T

SEQ. ID. NO. 40 C G A G C A G T G A T T A T G T T T G C C A A T G
 SEQ. ID. NO. 46 C G G G A G C T G C T T G C T G C C A G C C A G C
 SEQ. ID. NO. 36 C G G G A G C T G C T T G C T G C C A G C C A G C
 SEQ. ID. NO. 32 C T T G A G C C C C T C A T C A A G G A G A T T G

SEQ. ID. NO. 40 A G G A T G A C A T C A G G A G G A T A T T G G A
 SEQ. ID. NO. 46 G C C T C A A T G C C A G C T T C A C C T G G G T
 SEQ. ID. NO. 36 G C C T C A A T G C C A G C T T C A C C T G G G T
 SEQ. ID. NO. 32 T C C G G C G C A A T A T C A C G G G C A A G A T

SEQ. ID. NO. 40 A G C A G C A A A A A A A C T A A A C C A A A G T
 SEQ. ID. NO. 46 G G C C A G T G A T G G T T G G G G G G C C C T G
 SEQ. ID. NO. 36 G G C C A G T G A T G G T T G G G G G G C C C T G
 SEQ. ID. NO. 32 C T G G C T G G C C A G C G A G G C C T G G G C C

SEQ. ID. NO. 40 G G G C A T T T T C T C T G G A T T G G C T C A G
 SEQ. ID. NO. 46 G A G A G T G T G G T G G C A G G C A G T G A G G
 SEQ. ID. NO. 36 G A G A G T G T G G T G G C A G G C A G T G A G G
 SEQ. ID. NO. 32 A G C T C C T C C C T G A T C G C C A T G C C T C

SEQ. ID. NO. 40 A T A G T T G G G G A T C C A A A A T A G C A C C
 SEQ. ID. NO. 46 G G G C T G C T G A G G G T G C T A T C A C C A T
 SEQ. ID. NO. 36 G G G C T G C T G A G G G T G C T A T C A C C A T
 SEQ. ID. NO. 32 A G T A C T T C C A C G T G G T T G G C G G C A C

SEQ. ID. NO. 40 T G T C T A T C A G C A A G A G G A G A T T G C A
 SEQ. ID. NO. 46 C G A G C T G G C C T C C T A C C C C A T C A G T
 SEQ. ID. NO. 36 C G A G C T G G C C T C C T A C C C C A T C A G T
 SEQ. ID. NO. 32 C A T T G G A T T C G C T C T G A A G G C T G G G

SEQ. ID. NO. 40 G A A G G G G C T G T G A C A A T T T T G C C C A
 SEQ. ID. NO. 46 G A C T T T G C C T C C T A C T T C C A G A G C C
 SEQ. ID. NO. 36 G A C T T T G C C T C C T A C T T C C A G A G C C
 SEQ. ID. NO. 32 C A G A T C C C A G G C T T C C G G G A A T T C C

Figure 11e

SEQ. ID. NO. 40 A A C G A G C A T C A A T T G A T G G A T T T G A
 SEQ. ID. NO. 46 T G G A C C C T T G G A A C A A C A G C C G G A A
 SEQ. ID. NO. 36 T G G A C C C T T G G A A C A A C A G C C G G A A
 SEQ. ID. NO. 32 T G A A G A A G G T C C A T C C C A G G A A G T C

SEQ. ID. NO. 40 T C G A T A C T T T A G A A G C C G A A C T C T T
 SEQ. ID. NO. 46 C C C C T G G T T C C G T G A A T T C T G G G A G
 SEQ. ID. NO. 36 C C C C T G G T T C C G T G A A T T C T G G G A G
 SEQ. ID. NO. 32 T G T C C A C A A T G G T T T T G C C A A G G A G

SEQ. ID. NO. 40 G C C A A T A A T C G A A G A A A T G T G T G G T
 SEQ. ID. NO. 46 C A G A G G T T C C G C T G C A G C T T C C G G C
 SEQ. ID. NO. 36 C A G A G G T T C C G C T G C A G C T T C C G G C
 SEQ. ID. NO. 32 T T T T G G G A A G A A A C A T T T A A C T G C C

SEQ. ID. NO. 40 T T G C A G A A T T C T G G G A G G A G A A T T T
 SEQ. ID. NO. 46 A G C G A G A C T G C G C A G C C C A C T C T C T
 SEQ. ID. NO. 36 A G C G A G A C T G C G C A G C C C A C T C T C T
 SEQ. ID. NO. 32 A C C T C C A A G A A G G T G C A A A A G G A C C

SEQ. ID. NO. 40 T G G C T G C A A G T T A G G A T C A C A T G G G
 SEQ. ID. NO. 46 C C G G G C T G T G C C C T T T G A G C A G G A G
 SEQ. ID. NO. 36 C C G G G C T G T G C C C T T T G A G C A G G A G
 SEQ. ID. NO. 32 T T T A C C T G T G G A C A C C T T T C T G A G A

SEQ. ID. NO. 40 A A A A G G A A C A G T C A T A T A A A G A A A T
 SEQ. ID. NO. 46 T C C A A G A T C A T G T T T G T G G T C A A T G
 SEQ. ID. NO. 36 T C C A A G A T C A T G T T T G T G G T C A A T G
 SEQ. ID. NO. 32 G G T C A C G A A G A A A G T G G C G A C A G G T

SEQ. ID. NO. 40 G C A C A G G G C T G G A G C G A A T T G C T C G
 SEQ. ID. NO. 46 C A G T G T A C G C C A T G G C C C A T G C G C T
 SEQ. ID. NO. 36 C A G T G T A C G C C A T G G C C C A T G C G C T
 SEQ. ID. NO. 32 T T A G C A A C A G C T C G A C A G C C T T C C G

SEQ. ID. NO. 40 G G A T T C A T C T T A T G A A C A G G A A G G A
 SEQ. ID. NO. 46 C C A C A A C A T G C A C C G T G C C C T C T G C
 SEQ. ID. NO. 36 C C A C A A C A T G C A C C G T G C C C T C T G C
 SEQ. ID. NO. 32 A C C C C T C T G T A C A G G G G A T G A G A A C

Figure 11f

SEQ. ID. NO. 40 A A G G T C C A A T T T G T A A T T G A T G C T G
 SEQ. ID. NO. 46 C C C A A C A C C A C C C G G C T C T G T G A C G
 SEQ. ID. NO. 36 C C C A A C A C C A C C C G G C T C T G T G A C G
 SEQ. ID. NO. 32 A T C A G C A G T G T C G A G A C C C C T T A C A

SEQ. ID. NO. 40 T A T A T T C C A T G G C T T A C G C C C T G C A
 SEQ. ID. NO. 46 C G A T G C G G C C A G T T A A C G G G C G C C G
 SEQ. ID. NO. 36 C G A T G C G G C C A G T T A A C G G G C G C C G
 SEQ. ID. NO. 32 T A G A T T A C A C G C A T T T A C G G A T A T C

SEQ. ID. NO. 40 C A A T A T G C A C A A A G A T C T C T G C C C T
 SEQ. ID. NO. 46 C C T C T A C A A G G A C T T T G T G C T C A A C
 SEQ. ID. NO. 36 C C T C T A C A A G G A C T T T G T G C T C A A C
 SEQ. ID. NO. 32 C T A C A A T G T G T A C T T A G C A G T C T A C

SEQ. ID. NO. 40 G G A T A C A T T G G C C T T T G T C C A C G A A
 SEQ. ID. NO. 46 G T C A A G T T T G A T G C C C C C T T T C G C C
 SEQ. ID. NO. 36 G T C A A G T T T G A T G C C C C C T T T C G C C
 SEQ. ID. NO. 32 T C C A T T G C C C A C G C C T T G C A A G A T A

SEQ. ID. NO. 40 T G A G T A C C A T T G A T G G G A A A G A G C T
 SEQ. ID. NO. 46 C A G C T G A C A C C C A C A A T G A G G T C C G
 SEQ. ID. NO. 36 C A G C T G A C A C C C A C A A T G A G G T C C G
 SEQ. ID. NO. 32 T A T A T A C C T G C T T A C C T G G G A G A G G

SEQ. ID. NO. 40 A C T T G G T T A T A T T C G G G C T G T A A A T
 SEQ. ID. NO. 46 C T T T G A C C G C T T T G G T G A T G G T A T T
 SEQ. ID. NO. 36 C T T T G A C C G C T T T G G T G A T G G T A T T
 SEQ. ID. NO. 32 G C T C T T C A C C A A T G G C T C C T G T G C A

SEQ. ID. NO. 40 T T T A A T G G C A G T G C T G G C A C T C C T G
 SEQ. ID. NO. 46 G G C C G C T A C A A C A T C T T C A C C T A T C
 SEQ. ID. NO. 36 G G C C G C T A C A A C A T C T T C A C C T A T C
 SEQ. ID. NO. 32 G A C A T C A A G A A A G T T G A G G C G T G G C

SEQ. ID. NO. 40 T C A C T T T T A A T G A A A A C G G A G A T G C
 SEQ. ID. NO. 46 T G C G T G C A G G C A G T G G G C G C T A T C G
 SEQ. ID. NO. 36 T G C G T G C A G G C A G T G G G C G C T A T C G
 SEQ. ID. NO. 32 A G G T C C T G A A G C A C C T A C G G C A T C T

Figure 11g

SEQ. ID. NO. 40 TCCTGGACGTTATGATATCTTCCAG
 SEQ. ID. NO. 46 CTACCAGAAAGGTGGGCTACTGGGCA
 SEQ. ID. NO. 36 CTACCAGAAAGGTGGGCTACTGGGCA
 SEQ. ID. NO. 32 AAAC TTTACAAACAATA TGGGGGAG

SEQ. ID. NO. 40 TATCAAATAACCAACAAAAGCACAG
 SEQ. ID. NO. 46 GAAGGCTTTGACTCTGGACACCAGCC
 SEQ. ID. NO. 36 GAAGGCTTTGACTCTGGACACCAGCC
 SEQ. ID. NO. 32 CAGGTGACCTTTGATGAGTGTGGTG

SEQ. ID. NO. 40 AGTACAAAGTCAATCGGCCCACTGGAC
 SEQ. ID. NO. 46 TCATCCCATGGGCCCTCACCCCTCAGC
 SEQ. ID. NO. 36 TCATCCCATGGGCCCTCACCCCTCAGC
 SEQ. ID. NO. 32 ACCGTGGTGGGGAAC TATTCCATCAT

SEQ. ID. NO. 40 CAATCAGCTTTCATCTAAAAGTGGAA
 SEQ. ID. NO. 46 CGGCCCCCTTGCCCGCCTCTCGCTGC
 SEQ. ID. NO. 36 CGGCCCCCTTGCCCGCCTCTCGCTGC
 SEQ. ID. NO. 32 CAAC TGGCACCTCTCCCCAGAGGAT

SEQ. ID. NO. 40 GACATGCAAGTGGGCTCATAGAGAAC
 SEQ. ID. NO. 46 AGTGAGCCCTTGCCCTCCAGAAATGAGG
 SEQ. ID. NO. 36 AGTGAGCCCTTGCCCTCCAGAAATGAGG
 SEQ. ID. NO. 32 GGCTCCAATCGTGTTTAAAGGAAGTCG

SEQ. ID. NO. 40 ATACTCACCCGGCGTCTGTCTGCAG
 SEQ. ID. NO. 46 TGAAGAGTGTTGCAGCCGGGCGAAGT
 SEQ. ID. NO. 36 TGAAGAGTGTTGCAGCCGGGCGAAGT
 SEQ. ID. NO. 32 GGTATTACAAACGTCTATGCCAAGAA

SEQ. ID. NO. 40 CCTGCCGTGTAAAGCCAGGGGAGAGG
 SEQ. ID. NO. 46 CTGCTGCTGGCTCTTGCA TTCCGTGC
 SEQ. ID. NO. 36 CTGCTGCTGGCTCTTGCA TTCCGTGC
 SEQ. ID. NO. 32 GGGAGAAAGACTCTTTCATCAACGAG

SEQ. ID. NO. 40 AAGAAAACGGTGAAAGGGGTCCCTT
 SEQ. ID. NO. 46 CAGCCCTATGAGTACCGATTGGACG
 SEQ. ID. NO. 36 CAGCCCTATGAGTACCGATTGGACG
 SEQ. ID. NO. 32 GAGAAAATCCTGTGGAGTGGGTTCT

Figure 11h

SEQ. ID. NO. 40 G C T G C T G G C A C T G T G A A C G C T G T G A
 SEQ. ID. NO. 46 A A T T C A C T T G C G C T G A T T G T G G C C T
 SEQ. ID. NO. 36 A A T T C A C T T G C G C T G A T T G T G G C C T
 SEQ. ID. NO. 32 C C A G G G A G G T G C C C T T C T C C A A C T G

SEQ. ID. NO. 40 A G G T T A C A A C T A C C A G G T G G A T G A G
 SEQ. ID. NO. 46 G G G C T A C T G G C C C A A T G C C A G C C T G
 SEQ. ID. NO. 36 G G G C T A C T G G C C C A A T G C C A G C C T G
 SEQ. ID. NO. 32 C A G C C G A G A C T G C C T G G C A G G G A C C

SEQ. ID. NO. 40 C T G T C C T G T G A A C T T T G C C C T C T G G
 SEQ. ID. NO. 46 A C T G G C T G C T T C G A A C T G C C C C A G G
 SEQ. ID. NO. 36 A C T G G C T G C T T C G A A C T G C C C C A G G
 SEQ. ID. NO. 32 A G G A A A G G G A T C A T T G A G G G G G A G C

SEQ. ID. NO. 40 A T C A G A G A C C C A A C A T G A A C C G C A C
 SEQ. ID. NO. 46 A G T A C A T C C G C T G G G G C G A T G C C T G
 SEQ. ID. NO. 36 A G T A C A T C C G C T G G G G C G A T G C C T G
 SEQ. ID. NO. 32 C C A C C T G C T G C T T T G A G T G T G T G G A

SEQ. ID. NO. 40 A G G C T G C C A G C T T A T C C C C A T C A T C
 SEQ. ID. NO. 46 G G C T G T G G G A C C T G T C A C C A T C G C C
 SEQ. ID. NO. 36 G G C T G T G G G A C C T G T C A C C A T C G C C
 SEQ. ID. NO. 32 G T G T C C T G A T G G G G A G T A T A G T G A T

SEQ. ID. NO. 40 A A A T T G G A G T G G C A T T C T C C C T G G G
 SEQ. ID. NO. 46 T G C C T C G G T G C C C T G G C C A C C C T C T
 SEQ. ID. NO. 36 T G C C T C G G T G C C C T G G C C A C C C T C T
 SEQ. ID. NO. 32 G A G A C A G A T G C C A G T G C C T G T A A C A

SEQ. ID. NO. 40 C T G T G G T G C C T G T G T T T G T T G C A A T
 SEQ. ID. NO. 46 T T G T G C T G G G T G T C T T T G T G C G G C A
 SEQ. ID. NO. 36 T T G T G C T G G G T G T C T T T G T G C G G C A
 SEQ. ID. NO. 32 A G T G C C C A G A T G A C T T C T G G T C C A A

SEQ. ID. NO. 40 A T T G G G A A T C A T C G C C A C C A C C T T T
 SEQ. ID. NO. 46 C A A T G C C A C A C C A G T G G T C A A G G C C
 SEQ. ID. NO. 36 C A A T G C C A C A C C A G T G G T C A A G G C C
 SEQ. ID. NO. 32 T G A G A A C C A C A C C T C C T G C T T C G A A

Figure 11i

SEQ. ID. NO. 40 G T G A T C G T G A C C T T T G T C C G C T A T A
 SEQ. ID. NO. 46 T C A G G T C G G G A G C T C T G C T A C A T C C
 SEQ. ID. NO. 36 T C A G G T C G G G A G C T C T G C T A C A T C C
 SEQ. ID. NO. 32 C T G C C C C A G G A G T A C A T C C G C T G G G

SEQ. ID. NO. 40 A T G A C A C A C C T A T C G T G A G G G C T T C
 SEQ. ID. NO. 46 T G C T G G G T G G T G T C T T C C T C T G C T A
 SEQ. ID. NO. 36 T G C T G G G T G G T G T C T T C C T C T G C T A
 SEQ. ID. NO. 32 G C G A T G C C T G G G C T G T G G G A C C T G T

SEQ. ID. NO. 40 A G G A C G C G A A C T T A G T T A C G T G C T C
 SEQ. ID. NO. 46 C T G C A T G A C C T T C A T C T T C A T T G C C
 SEQ. ID. NO. 36 C T G C A T G A C C T T C A T C T T C A T T G C C
 SEQ. ID. NO. 32 C A C C A T C G C C T G C C T C G G T G C C C T G

SEQ. ID. NO. 40 C T A A C G G G G A T T T T T C T C T G T T A T T
 SEQ. ID. NO. 46 A A G C C A T C C A C G G C A G T G T G T A C C T
 SEQ. ID. NO. 36 A A G C C A T C C A C G G C A G T G T G T A C C T
 SEQ. ID. NO. 32 G C C A C C C T G T T T G T G C T G G G T G T C T

SEQ. ID. NO. 40 C A A T C A C G T T T T T A A T G A T T G C A G C
 SEQ. ID. NO. 46 T A C G G C G T C T T G G T T T G G G C A C T G C
 SEQ. ID. NO. 36 T A C G G C G T C T T G G T T T G G G C A C T G C
 SEQ. ID. NO. 32 T T G T G C G G C A C A A T G C C A C A C C A G T

SEQ. ID. NO. 40 A C C A G A T A C A A T C A T A T G C T C C T T C
 SEQ. ID. NO. 46 C T T C T C T G T C T G C T A C T C A G C C C T G
 SEQ. ID. NO. 36 C T T C T C T G T C T G C T A C T C A G C C C T G
 SEQ. ID. NO. 32 G G T C A A G G C C T C A G G T C G G G A G C T C

SEQ. ID. NO. 40 C G A C G G G T C T T C C T A G G A C T T G G C A
 SEQ. ID. NO. 46 C T C A C C A A G A C C A A C C G C A T T G C A C
 SEQ. ID. NO. 36 C T C A C C A A G A C C A A C C G C A T T G C A C
 SEQ. ID. NO. 32 T G C T A C A T C C T G C T G G G T G G T G T C T

SEQ. ID. NO. 40 T G T G T T T C A G C T A T G C A G C C C T T C T
 SEQ. ID. NO. 46 G C A T C T T C G G T G G G G C C C G G G A G G G
 SEQ. ID. NO. 36 G C A T C T T C G G T G G G G C C C G G G A G G G
 SEQ. ID. NO. 32 T C C T C T G C T A C T G C A T G A C C T T C A T

Figure 11j

SEQ. ID. NO. 40 G A C C A A A A C A A A C C G T A T C C A C C G A
 SEQ. ID. NO. 46 T G C C C A G C G G C C A C G C T T C A T C A G T
 SEQ. ID. NO. 36 T G C C C A G C G G C C A C G C T T C A T C A G T
 SEQ. ID. NO. 32 C T T C A T T G C C A A G C C A T C C A C G G C A

SEQ. ID. NO. 40 A T A T T T G A G C A G G G G A A G A A A T C T G
 SEQ. ID. NO. 46 C C T G C C T C A C A G G T G G C C A T C T G C C
 SEQ. ID. NO. 36 C C T G C C T C A C A G G T G G C C A T C T G C C
 SEQ. ID. NO. 32 G T G T G T A C C T T A C G G C G T C T T G G T T

SEQ. ID. NO. 40 T C A C A G C G C C C A A G T T C A T T A G T C C
 SEQ. ID. NO. 46 T G G C A C T T A T C T C G G G C C A G C T G C T
 SEQ. ID. NO. 36 T G G C A C T T A T C T C G G G C C A G C T G C T
 SEQ. ID. NO. 32 T G G G C A C T G C C T T C T C T G T C T G C T A

SEQ. ID. NO. 40 A G C A T C T C A G C T G G T G A T C A C C T T C
 SEQ. ID. NO. 46 C A T C G T G G T C G C C T G G C T G G T G G T G
 SEQ. ID. NO. 36 C A T C G T G G T C G C C T G G C T G G T G G T G
 SEQ. ID. NO. 32 C T C A G C C C T G C T C A C C A A G A C C A A C

SEQ. ID. NO. 40 A G C C T C A T C T C C G T C C A G C T C C T T G
 SEQ. ID. NO. 46 G A G G C A C C G G G C A C A G G C A A G G A G A
 SEQ. ID. NO. 36 G A G G C A C C G G G C A C A G G C A A G G A G A
 SEQ. ID. NO. 32 C G C A T T G C A C G C A T C T T C G G T G G G G

SEQ. ID. NO. 40 G A G T G T T T G T C T G G T T T G T T G T G G A
 SEQ. ID. NO. 46 C A G C C C C C G A A C G G C G G G A G G T G G T
 SEQ. ID. NO. 36 C A G C C C C C G A A C G G C G G G A G G T G G T
 SEQ. ID. NO. 32 C C C G G G A G G G T G C C C A G C G G C C A C G

SEQ. ID. NO. 40 T C C C C C C C A C A T C A T C A T T G A C T A T
 SEQ. ID. NO. 46 G A C A C T G C G C T G C A A C C A C C G C G A T
 SEQ. ID. NO. 36 G A C A C T G C G C T G C A A C C A C C G C G A T
 SEQ. ID. NO. 32 C T T C A T C A G T C C T G C C T C A C A G G T G

SEQ. ID. NO. 40 G G A G A G C A G C G G A C A C T A G A T C C A G
 SEQ. ID. NO. 46 G C A A G T A T G T T G G G C T C G C T G G C C T
 SEQ. ID. NO. 36 G C A A G T A T G T T G G G C T C G C T G G C C T
 SEQ. ID. NO. 32 G C C A T C T G C C T G G C A C T T A T C T C G G

Figure 11k

SEQ. ID. NO. 40 A G A A G G C C A G G G G A G T G C T C A A G T G
 SEQ. ID. NO. 46 A C A A T G T G C T C C T C A T C G C G C T C T G
 SEQ. ID. NO. 36 A C A A T G T G C T C C T C A T C G C G C T C T G
 SEQ. ID. NO. 32 G C C A G C T G C T C A T C G T G G T C G C C T G

SEQ. ID. NO. 40 T G A C A T T T C T G A T C T C T C A C T C A T T
 SEQ. ID. NO. 46 C A C G C T T T A T G C C T T C A A G A C T C G C
 SEQ. ID. NO. 36 C A C G C T T T A T G C C T T C A A G A C T C G C
 SEQ. ID. NO. 32 G C T G G T G G T G G A G G C A C C G G G C A C A

SEQ. ID. NO. 40 T G T T C A C T T G G A T A C A G T A T C C T C T
 SEQ. ID. NO. 46 A A G T G C C C C G A A A A C T T C A A C G A G G
 SEQ. ID. NO. 36 A A G T G C C C C G A A A A C T T C A A C G A G G
 SEQ. ID. NO. 32 G G C A A G G A G A C A G C C C C C G A A C G G C

SEQ. ID. NO. 40 T G A T G G T C A C T T G T A C T G T T T A T G C
 SEQ. ID. NO. 46 C C A A G T T C A T T G G C T T C A C C A T G T A
 SEQ. ID. NO. 36 C C A A G T T C A T T G G C T T C A C C A T G T A
 SEQ. ID. NO. 32 G G G A G G T G G T G A C A C T G C G C T G C A A

SEQ. ID. NO. 40 C A T T A A A A C G A G A G G T G T C C C A G A G
 SEQ. ID. NO. 46 C A C C A C C T G C A T C A T C T G G C T G G C A
 SEQ. ID. NO. 36 C A C C A C C T G C A T C A T C T G G C T G G C A
 SEQ. ID. NO. 32 C C A C C G C G A T G C A A G T A T G T T G G G C

SEQ. ID. NO. 40 A C T T T C A A T G A A G C C A A A C C T A T T G
 SEQ. ID. NO. 46 T T C C T G C C C A T C T T C T A T G T C A C C T
 SEQ. ID. NO. 36 T T C C T G C C C A T C T T C T A T G T C A C C T
 SEQ. ID. NO. 32 T C G C T G G C C T A C A A T G T G C T C C T C A

SEQ. ID. NO. 40 G A T T T A C C A T G T A T A C C A C C T G C A T
 SEQ. ID. NO. 46 C C A G T G A C T A C C G G G T A C A G A C C A C
 SEQ. ID. NO. 36 C C A G T G A C T A C C G G G T A C A G A C C A C
 SEQ. ID. NO. 32 T C G C G C T C T G C A C G C T T T A T G C C T T

SEQ. ID. NO. 40 C A T T T G G T T A G C T T T C A T C C C C A T C
 SEQ. ID. NO. 46 C A C C A T G T G C G T G T C A G T C A G C C T C
 SEQ. ID. NO. 36 C A C C A T G T G C G T G T C A G T C A G C C T C
 SEQ. ID. NO. 32 C A A T A C T C G C A A G T G C C C C G A A A A C

Figure 11L

SEQ. ID. NO. 40 T T T T T T G G T A C A G C C C A G T C A G C A G
 SEQ. ID. NO. 46 A G C G G C T C C G T G G T G C T T G G C T G C C
 SEQ. ID. NO. 36 A G C G G C T C C G T G G T G C T T G G C T G C C
 SEQ. ID. NO. 32 T T C A A C G A G G C C A A G T T C A T T G G C T

SEQ. ID. NO. 40 A A A A G A T G T A C A T C C A G A C A A C A A C
 SEQ. ID. NO. 46 T C T T T G C G C C C A A G C T G C A C A T C A T
 SEQ. ID. NO. 36 T C T T T G C G C C C A A G C T G C A C A T C A T
 SEQ. ID. NO. 32 T C A C C A T G T A C A C C A C C T G C A T C A T

SEQ. ID. NO. 40 A C T T A C T G T C T C C A T G A G T T T A A G T
 SEQ. ID. NO. 46 C C T C T T C C A G C C G C A G A A G A A C A C C
 SEQ. ID. NO. 36 C C T C T T C C A G C C G C A G A A G A A C A C C
 SEQ. ID. NO. 32 C T G G C T G G C A T T G T T G C C C A T C T T C

SEQ. ID. NO. 40 G C T T C A G T A T C T C T G G G C A T G C T C T
 SEQ. ID. NO. 46 A T C G A G G A G G T G C G T T G C A G C A C C G
 SEQ. ID. NO. 36 A T C G A G G A G G T G C G T T G C A G C A C C G
 SEQ. ID. NO. 32 T A T G T C A C C T C C A G T G A C T A C C G G G

SEQ. ID. NO. 40 A T A T G C C C A A G G T T T A T A T T A T A A T
 SEQ. ID. NO. 46 C A G C T C A C G C T T T C A A G G T G G C T G C
 SEQ. ID. NO. 36 C A G C T C A C G C T T T C A A G G T G G C T G C
 SEQ. ID. NO. 32 T A C A G A C C A C C A C C A T G T G C G T G T C

SEQ. ID. NO. 40 T T T T C A T C C A G A A C A G A A T A C C A T C
 SEQ. ID. NO. 46 C C G G G C C A C G C T G C G C C G C A G C A A C
 SEQ. ID. NO. 36 C C G G G C C A C G C T G C G C C G C A G C A A C
 SEQ. ID. NO. 32 A G T C A G C C T C A G C G G C T C C G T G G T G

SEQ. ID. NO. 40 G A G G A G G T G C G T T G C A G C A C C G C A G
 SEQ. ID. NO. 46 G T C T C C C G C A A G C G G T C C A G C A G C C
 SEQ. ID. NO. 36 G T C T C C C G C A A G C G G T C C A G C A G C C
 SEQ. ID. NO. 32 C T T G G C T G C C T C T T T G C G C C C A A G C

SEQ. ID. NO. 40 C T C A C G C T T T C A A G G T G G C T G C C C G
 SEQ. ID. NO. 46 T T G G A G G C T C C A C G G G A T C C A C C C C
 SEQ. ID. NO. 36 T T G G A G G C T C C A C G G G A T C C A C C C C
 SEQ. ID. NO. 32 T G C A C A T C A T C C T C T T C C A G C C G C A

Figure 11m

SEQ. ID. NO. 40 G G C C A C G C T G C G C C G C A G C A A C G T C
 SEQ. ID. NO. 46 C T C C T C C T C C A T C A G C A G C A A G A G C
 SEQ. ID. NO. 36 C T C C T C C T C C A T C A G C A G C A A G A G C
 SEQ. ID. NO. 32 G A A G A A C G T G G T T A G C C A C C G G G C A

SEQ. ID. NO. 40 T C C C G C A A G C G G T C C A G C A G C C T T G
 SEQ. ID. NO. 46 A A C A G C G A A G A C C C A T T C C C A C A G C
 SEQ. ID. NO. 36 A A C A G C G A A G A C C C A T T C C C A C A G C
 SEQ. ID. NO. 32 C C C A C C A G C C G C T T T G G C A G T G C T G

SEQ. ID. NO. 40 G A G G C T C C A C G G G A T C C A C C C C C T C
 SEQ. ID. NO. 46 C C G A G A G G C A G A A A G C A G C A G C A G C C
 SEQ. ID. NO. 36 C C G A G A G G C A G A A A G C A G C A G C A G C C
 SEQ. ID. NO. 32 C T G C C A G G G C C A G C T C C A G C C T T G G

SEQ. ID. NO. 40 C T C C T C C A T C A G C A G C A A G A G C A A C
 SEQ. ID. NO. 46 G C T G G C C C T A A C C C A G C A A G A G C A G
 SEQ. ID. NO. 36 G C T G G C C C T A A C C C A G C A A G A G C A G
 SEQ. ID. NO. 32 C C A A G G G T C T G G C T C C C A G T T T G T C

SEQ. ID. NO. 40 A G C G A A G A C C C A T T C C C A C A G C C C G
 SEQ. ID. NO. 46 C A G C A G C A G C C C C T G A C C C T C C C A C
 SEQ. ID. NO. 36 C A G C A G C A G C C C C T G A C C C T C C C A C
 SEQ. ID. NO. 32 C C C A C T G T T T G C A A T G G C C G T G A G G

SEQ. ID. NO. 40 A G A G G C A G A A A G C A G C A G C A G C C G C T
 SEQ. ID. NO. 46 A G C A G C A A C G A T C T C A G C A G C A G C C
 SEQ. ID. NO. 36 A G C A G C A A C G A T C T C A G C A G C A G C C
 SEQ. ID. NO. 32 T G G T G G A C T C G A C A A A C G T C A T C G C T

SEQ. ID. NO. 40 G G C C C T A A C C C A G C A A A G A G C A G C A G
 SEQ. ID. NO. 46 C A G A T G C A A A G C A G A A A G G T C A T C T T T
 SEQ. ID. NO. 36 C A G A T G C A A A G C A G A A A G G T C A T C T T T
 SEQ. ID. NO. 32 T A T G A C T C T G G A G T C C A T C A T G G C G

SEQ. ID. NO. 40 C A G C A G C C C C T G A C C C T C C C A C A G C
 SEQ. ID. NO. 46 G G C A G C G G C A C G G T C A C C T T C T C A C
 SEQ. ID. NO. 36 G G C A G C G G C A C G G T C A C C T T C T C A C
 SEQ. ID. NO. 32 T G C T G C C T G A G C G A G G A G G C C A A G G

Figure 11n

SEQ. ID. NO. 40 A G C A A C G A T C T C A G C A G C A G C C C A G
 SEQ. ID. NO. 46 T G A G C T T T G A T G A G C C T C A G A A G A A
 SEQ. ID. NO. 36 T G A G C T T T G A T G A G C C T C A G A A G A A
 SEQ. ID. NO. 32 A A G C C C G G C G G A T C A A C G A C G A G A T

SEQ. ID. NO. 40 A T G C A A G C A G A A G G T C A T C T T T G G C
 SEQ. ID. NO. 46 C G C C A T G G C C C A C G G G A A T T C T A C G
 SEQ. ID. NO. 36 C G C C A T G G C C C A C G G G A A T T C T A C G
 SEQ. ID. NO. 32 C G A G C G G C A G C T C C G C A G G G A C A A G

SEQ. ID. NO. 40 A G C G G C A C G G T C A C C T T C T C A C T G A
 SEQ. ID. NO. 46 C A C C A G A A C T C C C T G G A G G C C C A G A
 SEQ. ID. NO. 36 C A C C A G A A C T C C C T G G A G G C C C A G A
 SEQ. ID. NO. 32 C G G G A C G C C C G C C G G G A G C T C A A G C

SEQ. ID. NO. 40 G C T T T G A T G A G C C T C A G A A G A A C G C
 SEQ. ID. NO. 46 A A A G C A G C G A T A C G C T G A C C C G A C A
 SEQ. ID. NO. 36 A A A G C A G C G A T A C G C T G A C C C G A C A
 SEQ. ID. NO. 32 T G C T G C T G C T C G G G A C A G G A G A G A G

SEQ. ID. NO. 40 C A T G G C C C A C G G G A A T T C T A C G C A C
 SEQ. ID. NO. 46 C C A G C C A T T A C T C C C G C T G C A G T G C
 SEQ. ID. NO. 36 C C A G C C A T T A C T C C C G C T G C A G T G C
 SEQ. ID. NO. 32 T G G C A A G A G T A C G T T T A T C A A G C A G

SEQ. ID. NO. 40 C A G A A C T C C C T G G A G G C C C A G A A A A
 SEQ. ID. NO. 46 G G G G A A A C G G A C T T A G A T C T G A C C G
 SEQ. ID. NO. 36 G G G G A A A C G G A C T T A G A T C T G A C C G
 SEQ. ID. NO. 32 A T G A G A A T C A T C C A T G G G T C A G G A T

SEQ. ID. NO. 40 G C A G C G A T A C G C T G A C C C G A C A C C A
 SEQ. ID. NO. 46 T C C A G G A A A C A G G T C T G C A A G G A C C
 SEQ. ID. NO. 36 T C C A G G A A A C A G G T C T G C A A G G A C C
 SEQ. ID. NO. 32 A C T C T G A T G A A G A T A A A A G G G G C T T

SEQ. ID. NO. 40 G C C A T T A C T C C C G C T G C A G T G C G G G
 SEQ. ID. NO. 46 T G T G G G T G G A G A C C A G C G G C C A G A G
 SEQ. ID. NO. 36 T G T G G G T G G A G A C C A G C G G C C A G A G
 SEQ. ID. NO. 32 C A C C A A G C T G G T G T A T C A G A A C A T C

Figure 110

SEQ. ID. NO. 40 G A A A C G G A C T T A G A T C T G A C C G T C C
 SEQ. ID. NO. 46 G T G G A G G A C C C T G A A G A G T T G T C C C
 SEQ. ID. NO. 36 G T G G A G G A C C C T G A A G A G T T G T C C C
 SEQ. ID. NO. 32 T T C A C G G C C A T G C A G G C C A T G A T C A

SEQ. ID. NO. 40 A G G A A A C A G G T C T G C A A G G A C C T G T
 SEQ. ID. NO. 46 C A G C A C T T G T A G T G T C C A G T T C A C A
 SEQ. ID. NO. 36 C A G C A C T T G T A G T G T C C A G T T C A C A
 SEQ. ID. NO. 32 G A G C C A T G G A C A C A C T C A A G A T C C C

SEQ. ID. NO. 40 G G G T G G A G A C C A G C G G C C A G A G G T G
 SEQ. ID. NO. 46 G A G C T T T G T C A T C A G T G G T G G A G G C
 SEQ. ID. NO. 36 G A G C T T T G T C A T C A G T G G T G G A G G C
 SEQ. ID. NO. 32 A T A C A A G T A T G A G C A C A A T A A G G C T

SEQ. ID. NO. 40 G A G G A C C C T G A A G A G T T G T C C C C A G
 SEQ. ID. NO. 46 A G C A C T G T T A C A G A A A A C G T A G T G A
 SEQ. ID. NO. 36 A G C A C T G T T A C A G A A A A C G T A G T G A
 SEQ. ID. NO. 32 C A T G C A C A A T T A G T T C G A G A A G T T G

SEQ. ID. NO. 40 C A C T T G T A G T G T C C A G T T C A C A G A G
 SEQ. ID. NO. 46 A T T C A G C G G C C G C C A T G A C T C T G G A
 SEQ. ID. NO. 36 A T T C A A T G A C T C T G G A G T C C A T C A T
 SEQ. ID. NO. 32 A T G T G G A G A A G G T G T C T G C T T T T G A

SEQ. ID. NO. 40 C T T T G T C A T C A G T G G T G G A G G C A G C
 SEQ. ID. NO. 46 G T C C A T C A T G G C G T G C T G C C T G A G C
 SEQ. ID. NO. 36 G G C G T G C T G C C T G A G C G A G G A G G C C
 SEQ. ID. NO. 32 G A A T C C A T A T G T A G A T G C A A T A A A G

SEQ. ID. NO. 40 A C T G T T A C A G A A A A C G T A G T G A A T T
 SEQ. ID. NO. 46 G A G G A G G C C A A G G A A G C C C G G C G G A
 SEQ. ID. NO. 36 A A G G A A G C C C G G C G G A T C A A C G A C G
 SEQ. ID. NO. 32 A G T T T A T G G A A T G A T C C T G G A A T C C

SEQ. ID. NO. 40 C A - - - - -
 SEQ. ID. NO. 46 T C A A C G A C G A G A T C G A G C G G C A G C T
 SEQ. ID. NO. 36 A G A T C G A G C G G C A G C T C C G C A G G G A
 SEQ. ID. NO. 32 A G G A A T G C T A T G A T A G A C G A C G A G A

Figure 11p

SEQ. ID. NO. 40 - - - - -
 SEQ. ID. NO. 46 C C G C A G G G A C A A G C G G G A C G C C C G C
 SEQ. ID. NO. 36 C A A G C G G G A C G C C C G C C G G G A G C T C
 SEQ. ID. NO. 32 A T A T C A A T T A T C T G A C T C T A C C A A A

SEQ. ID. NO. 40 - - - - - A T G A C T C T G G
 SEQ. ID. NO. 46 C G G G A G C T C A A G C T G C T G C T G C T C G
 SEQ. ID. NO. 36 A A G C T G C T G C T G C T C G G G A C A G G A G
 SEQ. ID. NO. 32 T A C T A T C T T A A T G A C T T G G A C C G C G

SEQ. ID. NO. 40 A G T C C A T C A T G G C G T G C T G C C T G A G
 SEQ. ID. NO. 46 G G A C A G G A G A G A G T G G C A A G A G T A C
 SEQ. ID. NO. 36 A G A G T G G C A A G A G T A C G T T T A T C A A
 SEQ. ID. NO. 32 T A G C T G A C C C T G C C T A C C T G C C T A C

SEQ. ID. NO. 40 C G A G G A G G C C A A G G A A G C C C G G C G G
 SEQ. ID. NO. 46 G T T T A T C A A G C A G A T G A G A A T C A T C
 SEQ. ID. NO. 36 G C A G A T G A G A A T C A T C C A T G G G T C A
 SEQ. ID. NO. 32 G C A A C A A G A T G T G C T T A G A G T T C G A

SEQ. ID. NO. 40 A T C A A C G A C G A G A T C G A G C G G C A G C
 SEQ. ID. NO. 46 C A T G G G T C A G G A T A C T C T G A T G A A G
 SEQ. ID. NO. 36 G G A T A C T C T G A T G A A G A T A A A A G G G
 SEQ. ID. NO. 32 G T C C C C A C C A C A G G G A T C A T C G A A T

SEQ. ID. NO. 40 T C C G C A G G G A C A A G C G G G A C G C C C G
 SEQ. ID. NO. 46 A T A A A A G G G G C T T C A C C A A G C T G G T
 SEQ. ID. NO. 36 G C T T C A C C A A G C T G G T G T A T C A G A A
 SEQ. ID. NO. 32 A C C C C T T T G A C T T A C A A A G T G T C A T

SEQ. ID. NO. 40 C C G G G A G C T C A A G C T G C T G C T G C T C
 SEQ. ID. NO. 46 G T A T C A G A A C A T C T T C A C G G C C A T G
 SEQ. ID. NO. 36 C A T C T T C A C G G C C A T G C A G G C C A T G
 SEQ. ID. NO. 32 T T T C A G A A T G G T C G A T G T A G G G G G C

SEQ. ID. NO. 40 G G G A C A G G A G A G A G T G G C A A G A G T A
 SEQ. ID. NO. 46 C A G G C C A T G A T C A G A G C C A T G G A C A
 SEQ. ID. NO. 36 A T C A G A G C C A T G G A C A C A C T C A A G A
 SEQ. ID. NO. 32 C A A A G G T C A G A G A G A A G A A A A T G G A

Figure 11q

SEQ. ID. NO. 40 C G T T T A T C A A G C A G A T G A G A A T C A T
 SEQ. ID. NO. 46 C A C T C A A G A T C C C A T A C A A G T A T G A
 SEQ. ID. NO. 36 T C C C A T A C A A G T A T G A G C A C A A T A A
 SEQ. ID. NO. 32 T A C A C T G C T T T G A A A A T G T C A C C T C

SEQ. ID. NO. 40 C C A T G G G T C A G G A T A C T C T G A T G A A
 SEQ. ID. NO. 46 G C A C A A T A A G G C T C A T G C A C A A T T A
 SEQ. ID. NO. 36 G G C T C A T G C A C A A T T A G T T C G A G A A
 SEQ. ID. NO. 32 T A T C A T G T T T C T A G T A G C G C T T A G T

SEQ. ID. NO. 40 G A T A A A A G G G G C T T C A C C A A G C T G G
 SEQ. ID. NO. 46 G T T C G A G A A G T T G A T G T G G A G A A G G
 SEQ. ID. NO. 36 G T T G A T G T G G A G A A G G T G T C T G C T T
 SEQ. ID. NO. 32 G A A T A T G A T C A A G T T C T C G T G G A G T

SEQ. ID. NO. 40 T G T A T C A G A A C A T C T T C A C G G C C A T
 SEQ. ID. NO. 46 T G T C T G C T T T T G A G A A T C C A T A T G T
 SEQ. ID. NO. 36 T T G A G A A T C C A T A T G T A G A T G C A A T
 SEQ. ID. NO. 32 C A G A C A A T G A G A A C C G A A T G G A G G A

SEQ. ID. NO. 40 G C A G G C C A T G A T C A G A G C C A T G G A C
 SEQ. ID. NO. 46 A G A T G C A A T A A A G A G T T T A T G G A A T
 SEQ. ID. NO. 36 A A A G A G T T T A T G G A A T G A T C C T G G A
 SEQ. ID. NO. 32 A A G C A A G G C T C T C T T T A G A A C A A T T

SEQ. ID. NO. 40 A C A C T C A A G A T C C C A T A C A A G T A T G
 SEQ. ID. NO. 46 G A T C C T G G A A T C C A G G A A T G C T A T G
 SEQ. ID. NO. 36 A T C C A G G A A T G C T A T G A T A G A C G A C
 SEQ. ID. NO. 32 A T C A C A T A C C C C T G G T T C C A G A A C T

SEQ. ID. NO. 40 A G C A C A A T A A G G C T C A T G C A C A A T T
 SEQ. ID. NO. 46 A T A G A C G A C G A G A A T A T C A A T T A T C
 SEQ. ID. NO. 36 G A G A A T A T C A A T T A T C T G A C T C T A C
 SEQ. ID. NO. 32 C C T C G G T T A T T C T G T T C T T A A A C A A

SEQ. ID. NO. 40 A G T T C G A G A A G T T G A T G T G G A G A A G
 SEQ. ID. NO. 46 T G A C T C T A C C A A A T A C T A T C T T A A T
 SEQ. ID. NO. 36 C A A A T A C T A T C T T A A T G A C T T G G A C
 SEQ. ID. NO. 32 G A A A G A T C T T C T A G A G G A G A A A A T C

Figure 11r

SEQ. ID. NO. 40 GTGTCCTGCTTTTGTAGGAATCCATATG
 SEQ. ID. NO. 46 GACTTTGGACCGCGTAGCTGACCCCTG
 SEQ. ID. NO. 36 CGCGTAGCTGACCCCTGCCTACCTGC
 SEQ. ID. NO. 32 ATGTATTCCCATCTAGTCGACTACT

SEQ. ID. NO. 40 TAGATGCAATAAAGAGTTTATGGAA
 SEQ. ID. NO. 46 CCTACCTGCCTACGCAACAAGATGT
 SEQ. ID. NO. 36 CTACGCAACAAGATGTGCTTAGAGT
 SEQ. ID. NO. 32 TCC CAG AATAATGATGGACCC CAGAG

SEQ. ID. NO. 40 TGATCCTGGAATCCAGGAATGCTAT
 SEQ. ID. NO. 46 GCTTAGAGTTTCGAGTCCCCACCCACA
 SEQ. ID. NO. 36 TCGAGTCCCCACCCACAGGGATCATC
 SEQ. ID. NO. 32 AGATGCC CAGGCAGCCCCGAGAAATTC

SEQ. ID. NO. 40 GATAGACGACGAGGAATATCAATTAT
 SEQ. ID. NO. 46 GGGATCATCGAATAACCCCTTTGACT
 SEQ. ID. NO. 36 GAATAACCCCTTTGACTTACAAAGTG
 SEQ. ID. NO. 32 ATTCTGAAGATGTTTCGTGGACCTGA

SEQ. ID. NO. 40 CTGACTCTACCAAAATACTATCTTAA
 SEQ. ID. NO. 46 TACAAAGTGTCATTTTTCAGAAATGGT
 SEQ. ID. NO. 36 TCATTTTTCAGAAATGGTCGATGTAGG
 SEQ. ID. NO. 32 ACCCAGACAGTGACAAAAATTATCTA

SEQ. ID. NO. 40 TGACTTTGGACCGCGTAGCTGACCCCT
 SEQ. ID. NO. 46 CGATGTAGGGGGGCCAAAGGTCAGAG
 SEQ. ID. NO. 36 GGGCCCAAAGGTCAGAGAGAGAGAAAA
 SEQ. ID. NO. 32 CTC CCACTTCAACGTGCGCCACAGAC

SEQ. ID. NO. 40 GCCTACCTGCCTACGCAACAAGATG
 SEQ. ID. NO. 46 AGAAGAAAAATGGATACACTGCTTTTG
 SEQ. ID. NO. 36 TGGATACACTGCTTTTGAAAAATGTCA
 SEQ. ID. NO. 32 ACCGAGAAATATCCGCTTTTGTC TTG

SEQ. ID. NO. 40 TGCTTAGAGTTTCGAGTCCCCACCCAC
 SEQ. ID. NO. 46 AAAATGTCACTCTATCATGTTTCT
 SEQ. ID. NO. 36 CCTCTATCATGTTTCTAGTAGCGCT
 SEQ. ID. NO. 32 CTGCCGTCAAGGACACCATCCTCCA

Figure 11s

SEQ. ID. NO. 40 A G G G A T C A T C G A A T A C C C C T T T G A C
 SEQ. ID. NO. 46 A G T A G C G C T T A G T G A A T A T G A T C A A
 SEQ. ID. NO. 36 T A G T G A A T A T G A T C A A G T T C T C G T G
 SEQ. ID. NO. 32 G T T G A A C C T G A A G G A C T G C G G T C T G

SEQ. ID. NO. 40 T T A C A A A G T G T C A T T T T C A G A A T G G
 SEQ. ID. NO. 46 G T T C T C G T G G A G T C A G A C A A T G A G A
 SEQ. ID. NO. 36 G A G T C A G A C A A T G A G A A C C G A A T G G
 SEQ. ID. NO. 32 T T C T A A

SEQ. ID. NO. 40 T C G A T G T A G G G G G C C A A A G G T C A G A
 SEQ. ID. NO. 46 A C C G A A T G G A G G A A A G C A A G G C T C T
 SEQ. ID. NO. 36 A G G A A A G C A A G G C T C T C T T T A G A A C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A G A A G A A A A T G G A T A C A C T G C T T T
 SEQ. ID. NO. 46 C T T T A G A A C A A T T A T C A C A T A C C C C
 SEQ. ID. NO. 36 A A T T A T C A C A T A C C C C T G G T T C C A G
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A A A A T G T C A C C T C T A T C A T G T T T C
 SEQ. ID. NO. 46 T G G T T C C A G A A C T C C T C G G T T A T T C
 SEQ. ID. NO. 36 A A C T C C T C G G T T A T T C T G T T C T T A A
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 T A G T A G C G C T T A G T G A A T A T G A T C A
 SEQ. ID. NO. 46 T G T T C T T A A A C A A G A A A G A T C T T C T
 SEQ. ID. NO. 36 A C A A G A A A G A T C T T C T A G A G G A G A A
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 A G T T C T C G T G G A G T C A G A C A A T G A G
 SEQ. ID. NO. 46 A G A G G A G A A A A T C A T G T A T T C C C A T
 SEQ. ID. NO. 36 A A T C A T G T A T T C C C A T C T A G T C G A C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 A A C C G A A T G G A G G A A A G C A A G G C T C
 SEQ. ID. NO. 46 C T A G T C G A C T A C T T C C C A G A A T A T G
 SEQ. ID. NO. 36 T A C T T C C C A G A A T A T G A T G G A C C C C
 SEQ. ID. NO. 32

Figure 11t

SEQ. ID. NO. 40 T C T T T A G A A C A A T T A T C A C A T A C C C
 SEQ. ID. NO. 46 A T G G A C C C C A G A G A G A T G C C C A G G C
 SEQ. ID. NO. 36 A G A G A G A T G C C C A G G C A G C C C G A G A
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 C T G G T T C C A G A A C T C C T C G G T T A T T
 SEQ. ID. NO. 46 A G C C C G A G A A T T C A T T C T G A A G A T G
 SEQ. ID. NO. 36 A T T C A T T C T G A A G A T G T T C G T G G A C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 C T G T T C T T A A A C A A G A A A G A T C T T C
 SEQ. ID. NO. 46 T T C G T G G A C C T G A A C C C A G A C A G T G
 SEQ. ID. NO. 36 C T G A A C C C A G A C A G T G A C A A A A T T A
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 T A G A G G A G A A A A T C A T G T A T T C C C A
 SEQ. ID. NO. 46 A C A A A A T T A T C T A C T C C C A C T T C A C
 SEQ. ID. NO. 36 T C T A C T C C C A C T T C A C G T G C G C C A C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 T C T A G T C G A C T A C T T C C C A G A A T A T
 SEQ. ID. NO. 46 G T G C G C C A C A G A C A C C G A G A A T A T C
 SEQ. ID. NO. 36 A G A C A C C G A G A A T A T C C G C T T T G T C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A T G G A C C C C A G A G A G A T G C C C A G G
 SEQ. ID. NO. 46 C G C T T T G T C T T T G C T G C C G T C A A G G
 SEQ. ID. NO. 36 T T T G C T G C C G T C A A G G A C A C C A T C C
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 C A G C C C G A G A A T T C A T T C T G A A G A T
 SEQ. ID. NO. 46 A C A C C A T C C T C C A G T T G A A C C T G A A
 SEQ. ID. NO. 36 T C C A G T T G A A C C T G A A G G A C T G C G G
 SEQ. ID. NO. 32

SEQ. ID. NO. 40 G T T C G T G G A C C T G A A C C C A G A C A G T
 SEQ. ID. NO. 46 G G A C T G C G G T C T G T T C T A A T T G T G C
 SEQ. ID. NO. 36 T C T G T T C T A A
 SEQ. ID. NO. 32

Figure 11u

SEQ. ID. NO. 40 G A C A A A A T T A T C T A C T C C C A C T T C A
SEQ. ID. NO. 46 C T C C T A G A C A C C C G C C C T G C C C T T C
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C G T G C G C C A C A G A C A C C G A G A A T A T
SEQ. ID. NO. 46 C C T G G T
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C C G C T T T G T C T T T G C T G C C G T C A A G
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A C A C C A T C C T C C A G T T G A A C C T G A
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 A G G A C T G C G G T C T G T T C T A A
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

Figure 11v

ClustalW Formatted Alignments

SEQ. ID. NO. 41 M V C E G K R S A S C P C F F L L T A K F Y W I L
 SEQ. ID. NO. 47 M G S L L A L P A L L L L W G A V A E G P A K K V
 SEQ. ID. NO. 37 M G S L L A L P A L L L L W G A V A E G P A K K V
 SEQ. ID. NO. 33 M A F Y S C C W V L L A L T W H T S A Y G P D Q R

SEQ. ID. NO. 41 T M M Q R T H S Q E Y A H S I R V D G D I I L G G
 SEQ. ID. NO. 47 L T L E G D L V L G G L F P V H Q K G G P A E D C
 SEQ. ID. NO. 37 L T L E G D L V L G G L F P V H Q K G G P A E D C
 SEQ. ID. NO. 33 A Q K K G D I I L G G L F P I H F G V A A K D Q D

SEQ. ID. NO. 41 L F P V H A K G E R G V P C G E L K K E K G I H R
 SEQ. ID. NO. 47 G P V N E H R G I Q R L E A M L F A L D R I N R D
 SEQ. ID. NO. 37 G P V N E H R G I Q R L E A M L F A L D R I N R D
 SEQ. ID. NO. 33 L K S R P E S V E C I R Y N F R G F R W L Q A M I

SEQ. ID. NO. 41 L E A M L Y A I D Q I N K D P D L L S N I T L G V
 SEQ. ID. NO. 47 P H L L P G V R L G A H I L D S C S K D T H A L E
 SEQ. ID. NO. 37 P H L L P G V R L G A H I L D S C S K D T H A L E
 SEQ. ID. NO. 33 F A I E E I N S S P A L L P N L T L G Y R I F D T

SEQ. ID. NO. 41 R I L D T C S R D T Y A L E Q S L T F V Q A L I E
 SEQ. ID. NO. 47 Q A L D F V R A S L S R G A D G S R H I C P D G S
 SEQ. ID. NO. 37 Q A L D F V R A S L S R G A D G S R H I C P D G S
 SEQ. ID. NO. 33 C N T V S K A L E A T L S F V A Q N K I D S L N L

SEQ. ID. NO. 41 K D A S D V K C A N G D P P I F T K P D K I S G V
 SEQ. ID. NO. 47 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
 SEQ. ID. NO. 37 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
 SEQ. ID. NO. 33 D E F C N C S E H I P S T I A V V G A T G S G V S

SEQ. ID. NO. 41 I G A A A S S V S I M V A N I L R L F K I P Q I S
 SEQ. ID. NO. 47 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
 SEQ. ID. NO. 37 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
 SEQ. ID. NO. 33 T A V A N L L G L F Y I P Q V S Y A S S S R L L S

SEQ. ID. NO. 41 Y A S T A P E L S D N T R Y D F F S R V V P P D S
 SEQ. ID. NO. 47 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
 SEQ. ID. NO. 37 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
 SEQ. ID. NO. 33 N K N Q F K S F L R T I P N D E H Q A T A M A D I

Figure 12a

SEQ. ID. NO. 41 YQAQAMVDIVTALGWNYVSTLASEG
 SEQ. ID. NO. 47 FFNWTYVSTVASEGDYGETGIEAFE
 SEQ. ID. NO. 37 FFNWTYVSTVASEGDYGETGIEAFE
 SEQ. ID. NO. 33 IEYFRWNWVG TIAADDDYGRPGIEK

SEQ. ID. NO. 41 NYGESGV EAF TQISREIGGV CIAQS
 SEQ. ID. NO. 47 LEARARNICVATSEKVGGRAMSRAAF
 SEQ. ID. NO. 37 LEARARNICVATSEKVGGRAMSRAAF
 SEQ. ID. NO. 33 FREEAEERD ICIDFSELISQYSDEE

SEQ. ID. NO. 41 QKIPREPRPGEF EKIIKRLL ETPNA
 SEQ. ID. NO. 47 EGVV RALLQKPSARVAVL FTRSEDA
 SEQ. ID. NO. 37 EGVV RALLQKPSARVAVL FTRSEDA
 SEQ. ID. NO. 33 EIQHVV EVIQNSTAKVIVVFSSGPD

SEQ. ID. NO. 41 RAVIMFANEDDIRRI LEAAKKLNQS
 SEQ. ID. NO. 47 REL LAASQRLNASFTWV ASDGWGAL
 SEQ. ID. NO. 37 REL LAASQRLNASFTWV ASDGWGAL
 SEQ. ID. NO. 33 LEPLIKEIVRRNITGKIWLASEAWA

SEQ. ID. NO. 41 GHFLWIGSDSWGSKIAPVYQQEEIA
 SEQ. ID. NO. 47 ESVVAGSEGA AEGAITIELASYPIS
 SEQ. ID. NO. 37 ESVVAGSEGA AEGAITIELASYPIS
 SEQ. ID. NO. 33 SSSL IAMPQYFHVVG GTIGFALKAG

SEQ. ID. NO. 41 EGAVTILPKRASIDGFDRYFRSRTL
 SEQ. ID. NO. 47 DFASYFQS LDPWNN SRNPWFREFWE
 SEQ. ID. NO. 37 DFASYFQS LDPWNN SRNPWFREFWE
 SEQ. ID. NO. 33 QIPGFREF FLKKVHPRKSVHNGFAKE

SEQ. ID. NO. 41 ANNRRNVWF AEFEW EENFGCKLGSHG
 SEQ. ID. NO. 47 QRFRC SFRQRDCAAHSLRAVPFEQE
 SEQ. ID. NO. 37 QRFRC SFRQRDCAAHSLRAVPFEQE
 SEQ. ID. NO. 33 FWEETFNCHLQEGAKG PLPVDTFLR

SEQ. ID. NO. 41 KRN SHIKKCTGLERI ARDSSYEQEG
 SEQ. ID. NO. 47 SKIMFVVNAVYAMAHALHNMHRA LC
 SEQ. ID. NO. 37 SKIMFVVNAVYAMAHALHNMHRA LC
 SEQ. ID. NO. 33 GHEESGDRFSNSSSTAFRPLCTGDEN

Figure 12b

SEQ. ID. NO. 41 K V Q F V I D A V Y S M A Y A L H N M H K D L C P
 SEQ. ID. NO. 47 P N T T R L C D A M R P V N G R R L Y K D F V L N
 SEQ. ID. NO. 37 P N T T R L C D A M R P V N G R R L Y K D F V L N
 SEQ. ID. NO. 33 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y

SEQ. ID. NO. 41 G Y I G L C P R M S T I D G K E L L G Y I R A V N
 SEQ. ID. NO. 47 V K F D A P F R P A D T H N E V R F D R F G D G I
 SEQ. ID. NO. 37 V K F D A P F R P A D T H N E V R F D R F G D G I
 SEQ. ID. NO. 33 S I A H A L Q D I Y T C L P G R G L F T N G S C A

SEQ. ID. NO. 41 F N G S A G T P V T F N E N G D A P G R Y D I F Q
 SEQ. ID. NO. 47 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
 SEQ. ID. NO. 37 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
 SEQ. ID. NO. 33 D I K K V E A W Q V L K H L R H L N F T N N M G E

SEQ. ID. NO. 41 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E
 SEQ. ID. NO. 47 E G L T L D T S L I P W A S P S A G P L P A S R C
 SEQ. ID. NO. 37 E G L T L D T S L I P W A S P S A G P L P A S R C
 SEQ. ID. NO. 33 Q V T F D E C G D L V G N Y S I I N W H L S P E D

SEQ. ID. NO. 41 D M Q W A H R E H T H P A S V C S L P C K P G E R
 SEQ. ID. NO. 47 S E P C L Q N E V K S V Q P G E V C C W L C I P C
 SEQ. ID. NO. 37 S E P C L Q N E V K S V Q P G E V C C W L C I P C
 SEQ. ID. NO. 33 G S I V F K E V G Y Y N V Y A K K G E R L F I N E

SEQ. ID. NO. 41 K K T V K G V P C C W H C E R C E G Y N Y Q V D E
 SEQ. ID. NO. 47 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
 SEQ. ID. NO. 37 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
 SEQ. ID. NO. 33 E K I L W S G F S R E V P F S N C S R D C L A G T

SEQ. ID. NO. 41 L S C E L C P L D Q R P N M N R T G C Q L I P I I
 SEQ. ID. NO. 47 T G C F E L P Q E Y I R W G D A W A V G P V T I A
 SEQ. ID. NO. 37 T G C F E L P Q E Y I R W G D A W A V G P V T I A
 SEQ. ID. NO. 33 R K G I I E G E P T C C F E C V E C P D G E Y S D

SEQ. ID. NO. 41 K L E W H S P W A V V P V F V A I L G I I A T T F
 SEQ. ID. NO. 47 C L G A L A T L F V L G V F V R H N A T P V V K A
 SEQ. ID. NO. 37 C L G A L A T L F V L G V F V R H N A T P V V K A
 SEQ. ID. NO. 33 E T D A S A C N K C P D D F W S N E N H T S C F E

Figure 12c

SEQ. ID. NO. 41 V I V T F V R Y N D T P I V R A S G R E L S Y V L
 SEQ. ID. NO. 47 S G R E L C Y I L L G G V F L C Y C M T F I F I A
 SEQ. ID. NO. 37 S G R E L C Y I L L G G V F L C Y C M T F I F I A
 SEQ. ID. NO. 33 L P Q E Y I R W G D A W A V G P V T I A C L G A L

SEQ. ID. NO. 41 L T G I F L C Y S I T F L M I A A P D T I I C S F
 SEQ. ID. NO. 47 K P S T A V C T L R R L G L G T A F S V C Y S A L
 SEQ. ID. NO. 37 K P S T A V C T L R R L G L G T A F S V C Y S A L
 SEQ. ID. NO. 33 A T L F V L G V F V R H N A T P V V K A S G R E L

SEQ. ID. NO. 41 R R V F L G L G M C F S Y A A L L T K T N R I H R
 SEQ. ID. NO. 47 L T K T N R I A R I F G G A R E G A Q R P R F I S
 SEQ. ID. NO. 37 L T K T N R I A R I F G G A R E G A Q R P R F I S
 SEQ. ID. NO. 33 C Y I L L G G V F L C Y C M T F I F I A K P S T A

SEQ. ID. NO. 41 I F E Q G K K S V T A P K F I S P A S Q L V I T F
 SEQ. ID. NO. 47 P A S Q V A I C L A L I S G Q L L I V V A W L V V
 SEQ. ID. NO. 37 P A S Q V A I C L A L I S G Q L L I V V A W L V V
 SEQ. ID. NO. 33 V C T L R R L G L G T A F S V C Y S A L L T K T N

SEQ. ID. NO. 41 S L I S V Q L L G V F V W F V V D P P H I I I D Y
 SEQ. ID. NO. 47 E A P G T G K E T A P E R R E V V T L R C N H R D
 SEQ. ID. NO. 37 E A P G T G K E T A P E R R E V V T L R C N H R D
 SEQ. ID. NO. 33 R I A R I F G G A R E G A Q R P R F I S P A S Q V

SEQ. ID. NO. 41 G E Q R T L D P E K A R G V L K C D I S D L S L I
 SEQ. ID. NO. 47 A S M L G S L A Y N V L L I A L C T L Y A F K T R
 SEQ. ID. NO. 37 A S M L G S L A Y N V L L I A L C T L Y A F K T R
 SEQ. ID. NO. 33 A I C L A L I S G Q L L I V V A W L V V E A P G T

SEQ. ID. NO. 41 C S L G Y S I L L M V T C T V Y A I K T R G V P E
 SEQ. ID. NO. 47 K C P E N F N E A K F I G F T M Y T T C I I W L A
 SEQ. ID. NO. 37 K C P E N F N E A K F I G F T M Y T T C I I W L A
 SEQ. ID. NO. 33 G K E T A P E R R E V V T L R C N H R D A S M L G

SEQ. ID. NO. 41 T F N E A K P I G F T M Y T T C I I W L A F I P I
 SEQ. ID. NO. 47 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
 SEQ. ID. NO. 37 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
 SEQ. ID. NO. 33 S L A Y N V L L I A L C T L Y A F N T R K C P E N

Figure 12d

SEQ. ID. NO. 41 F F G T A Q S A E K M Y I Q T T T L T V S M S L S
 SEQ. ID. NO. 47 S G S V V L G C L F A P K L H I I L F Q P Q K N T
 SEQ. ID. NO. 37 S G S V V L G C L F A P K L H I I L F Q P Q K N T
 SEQ. ID. NO. 33 F N E A K F I G F T M Y T T C I I W L A L L P I F

SEQ. ID. NO. 41 A S V S L G M L Y M P K V Y I I I F H P E Q N T I
 SEQ. ID. NO. 47 I E E V R C S T A A H A F K V A A R A T L R R S N
 SEQ. ID. NO. 37 I E E V R C S T A A H A F K V A A R A T L R R S N
 SEQ. ID. NO. 33 Y V T S S D Y R V Q T T T M C V S V S L S G S V V

SEQ. ID. NO. 41 E E V R C S T A A H A F K V A A R A T L R R S N V
 SEQ. ID. NO. 47 V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 37 V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 33 L G C L F A P K L H I I L F Q P Q K N V V S H R A

SEQ. ID. NO. 41 S R K R S S S L G G S T G S T P S S S I S S K S N
 SEQ. ID. NO. 47 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
 SEQ. ID. NO. 37 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
 SEQ. ID. NO. 33 P T S R F G S A A A R A S S S L G Q G S G S Q F V

SEQ. ID. NO. 41 S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q
 SEQ. ID. NO. 47 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
 SEQ. ID. NO. 37 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
 SEQ. ID. NO. 33 P T V C N G R E V V D S T T S S L M T L E S I M A

SEQ. ID. NO. 41 Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F G
 SEQ. ID. NO. 47 G S G T V T F S L S F D E P Q K N A M A H G N S T
 SEQ. ID. NO. 37 G S G T V T F S L S F D E P Q K N A M A H G N S T
 SEQ. ID. NO. 33 C C L S E E A K E A R R I N D E I E R Q L R R D K

SEQ. ID. NO. 41 S G T V T F S L S F D E P Q K N A M A H G N S T H
 SEQ. ID. NO. 47 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
 SEQ. ID. NO. 37 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
 SEQ. ID. NO. 33 R D A R R E L K L L L L G T G E S G K S T F I K Q

SEQ. ID. NO. 41 Q N S L E A Q K S S D T L T R H Q P L L P L Q C G
 SEQ. ID. NO. 47 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
 SEQ. ID. NO. 37 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
 SEQ. ID. NO. 33 M R I I H G S G Y S D E D K R G F T K L V Y Q N I

Figure 12e

SEQ. ID. NO. 41 E T D L D L T V Q E T G L Q G P V G G D Q R P E V
 SEQ. ID. NO. 47 V E D P E E L S P A L V V S S S Q S F V I S G G G
 SEQ. ID. NO. 37 V E D P E E L S P A L V V S S S Q S F V I S G G G
 SEQ. ID. NO. 33 F T A M Q A M I R A M D T L K I P Y K Y E H N K A

SEQ. ID. NO. 41 E D P E E L S P A L V V S S S Q S F V I S G G G S
 SEQ. ID. NO. 47 S T V T E N V V N S A A A M T L E S I M A C C L S
 SEQ. ID. NO. 37 S T V T E N V V N S M T L E S I M A C C L S E E A
 SEQ. ID. NO. 33 H A Q L V R E V D V E K V S A F E N P Y V D A I K

SEQ. ID. NO. 41 T V T E N V V N S M T L E S I M A C C L S E E A K
 SEQ. ID. NO. 47 E E A K E A R R I N D E I E R Q L R R D K R D A R
 SEQ. ID. NO. 37 K E A R R I N D E I E R Q L R R D K R D A R R E L
 SEQ. ID. NO. 33 S L W N D P G I Q E C Y D R R R E Y Q L S D S T K

SEQ. ID. NO. 41 E A R R I N D E I E R Q L R R D K R D A R R E L K
 SEQ. ID. NO. 47 R E L K L L L L G T G E S G K S T F I K Q M R I I
 SEQ. ID. NO. 37 K L L L L G T G E S G K S T F I K Q M R I I H G S
 SEQ. ID. NO. 33 Y Y L N D L D R V A D P A Y L P T Q Q D V L R V R

SEQ. ID. NO. 41 L L L L G T G E S G K S T F I K Q M R I I H G S G
 SEQ. ID. NO. 47 H G S G Y S D E D K R G F T K L V Y Q N I F T A M
 SEQ. ID. NO. 37 G Y S D E D K R G F T K L V Y Q N I F T A M Q A M
 SEQ. ID. NO. 33 V P T T G I I E Y P F D L Q S V I F R M V D V G G

SEQ. ID. NO. 41 Y S D E D K R G F T K L V Y Q N I F T A M Q A M I
 SEQ. ID. NO. 47 Q A M I R A M D T L K I P Y K Y E H N K A H A Q L
 SEQ. ID. NO. 37 I R A M D T L K I P Y K Y E H N K A H A Q L V R E
 SEQ. ID. NO. 33 Q R S E R R K W I H C F E N V T S I M F L V A L S

SEQ. ID. NO. 41 R A M D T L K I P Y K Y E H N K A H A Q L V R E V
 SEQ. ID. NO. 47 V R E V D V E K V S A F E N P Y V D A I K S L W N
 SEQ. ID. NO. 37 V D V E K V S A F E N P Y V D A I K S L W N D P G
 SEQ. ID. NO. 33 E Y D Q V L V E S D N E N R M E E S K A L F R T I

SEQ. ID. NO. 41 D V E K V S A F E N P Y V D A I K S L W N D P G I
 SEQ. ID. NO. 47 D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N
 SEQ. ID. NO. 37 I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D
 SEQ. ID. NO. 33 I T Y P W F Q N S S V I L F L N K K D L L E E K I

Figure 12f

SEQ. ID. NO. 41 Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R
 SEQ. ID. NO. 47 D L D R V A D P A Y L P T Q Q D V L R V R V P T T
 SEQ. ID. NO. 37 R V A D P A Y L P T Q Q D V L R V R V P T T G I I
 SEQ. ID. NO. 33 M Y S H L V D Y F P E Y D G P Q R D A Q A A R E F

SEQ. ID. NO. 41 V A D P A Y L P T Q Q D V L R V R V P T T G I I E
 SEQ. ID. NO. 47 G I I E Y P F D L Q S V I F R M V D V G G Q R S E
 SEQ. ID. NO. 37 E Y P F D L Q S V I F R M V D V G G Q R S E R R K
 SEQ. ID. NO. 33 I L K M F V D L N P D S D K I I Y S H F T C A T D

SEQ. ID. NO. 41 Y P F D L Q S V I F R M V D V G G Q R S E R R K W
 SEQ. ID. NO. 47 R R K W I H C F E N V T S I M F L V A L S E Y D Q
 SEQ. ID. NO. 37 W I H C F E N V T S I M F L V A L S E Y D Q V L V
 SEQ. ID. NO. 33 T E N I R F V F A A V K D T I L Q L N L K D C G L

SEQ. ID. NO. 41 I H C F E N V T S I M F L V A L S E Y D Q V L V E
 SEQ. ID. NO. 47 V L V E S D N E N R M E E S K A L F R T I I T Y P
 SEQ. ID. NO. 37 E S D N E N R M E E S K A L F R T I I T Y P W F Q
 SEQ. ID. NO. 33 F

SEQ. ID. NO. 41 S D N E N R M E E S K A L F R T I I T Y P W F Q N
 SEQ. ID. NO. 47 W F Q N S S V I L F L N K K D L L E E K I M Y S H
 SEQ. ID. NO. 37 N S S V I L F L N K K D L L E E K I M Y S H L V D
 SEQ. ID. NO. 33

SEQ. ID. NO. 41 S S V I L F L N K K D L L E E K I M Y S H L V D Y
 SEQ. ID. NO. 47 L V D Y F P E Y D G P Q R D A Q A A R E F I L K M
 SEQ. ID. NO. 37 Y F P E Y D G P Q R D A Q A A R E F I L K M F V D
 SEQ. ID. NO. 33

SEQ. ID. NO. 41 F P E Y D G P Q R D A Q A A R E F I L K M F V D L
 SEQ. ID. NO. 47 F V D L N P D S D K I I Y S H F T C A T D T E N I
 SEQ. ID. NO. 37 L N P D S D K I I Y S H F T C A T D T E N I R F V
 SEQ. ID. NO. 33

SEQ. ID. NO. 41 N P D S D K I I Y S H F T C A T D T E N I R F V F
 SEQ. ID. NO. 47 R F V F A A V K D T I L Q L N L K D C G L F
 SEQ. ID. NO. 37 F A A V K D T I L Q L N L K D C G L F
 SEQ. ID. NO. 33

Figure 12g

SEQ. ID. NO. 41 A A V K D T I L Q L N L K D C G L F
SEQ. ID. NO. 47
SEQ. ID. NO. 37
SEQ. ID. NO. 33

Figure 12h

ClustalW Formatted Alignments

SEQ. ID. NO. 44 A T G T T G C T G C T G C T A C T G G C G C
SEQ. ID. NO. 42 A T G G C T T C C C C G C G G A G C T C C G G G C

SEQ. ID. NO. 44 C A C T C T T C C T C C G C C C C C G G G C G C
SEQ. ID. NO. 42 A G C C C G G G C C G C C G C C G C C G C C G C C

SEQ. ID. NO. 44 G G G C G G G G C G C A G A C C C C C A A C G C C
SEQ. ID. NO. 42 A C C G C C G C C C G C G C G C C T G C T A C T G

SEQ. ID. NO. 44 A C C T C A G A A G G T T G C C A G A T C A T A C
SEQ. ID. NO. 42 C T A C T G C T G C T G C C G C T G C T G C T G C

SEQ. ID. NO. 44 A C C C G C C C T G G G A A G G G G G C A T C A G
SEQ. ID. NO. 42 C T C T G G C G C C C G G G G C C T G G G G C T G

SEQ. ID. NO. 44 G T A C C G G G G C C T G A C T C G G G A C C A G
SEQ. ID. NO. 42 G G C G C G G G G C G C C C C C C G G C C G C C G

SEQ. ID. NO. 44 G T G A A G G C T A T C A A C T T C C T G C C A G
SEQ. ID. NO. 42 C C C A G C A G C C C G C C G C T C T C C A T C A

SEQ. ID. NO. 44 T G G A C T A T G A G A T T G A G T A T G T G T G
SEQ. ID. NO. 42 T G G G C C T C A T G C C G C T C A C C A A G G A

SEQ. ID. NO. 44 C C G G G G G G A G C G C G A G G T G G T G G G G
SEQ. ID. NO. 42 G G T G G C C A A G G G C A G C A T C G G G C G C

SEQ. ID. NO. 44 C C C A A G G T C C G C A A G T G C C T G G C C A
SEQ. ID. NO. 42 G G T G T G C T C C C C G C C G T G G A A C T G G

SEQ. ID. NO. 44 A C G G C T C C T G G A C A G A T A T G G A C A C
SEQ. ID. NO. 42 C C A T C G A G C A G A T C C G C A A C G A G T C

SEQ. ID. NO. 44 A C C C A G C C G C T G T G T C C G A A T C T G C
SEQ. ID. NO. 42 A C T C C T G C G C C C T T A C T T C C T C G A C

Figure 13a

SEQ. ID. NO. 44 T C C A A G T C T T A T T T G A C C C T G G A A A
SEQ. ID. NO. 42 C T G C G G C T C T A T G A C A C G G A G T G C G

SEQ. ID. NO. 44 A T G G G A A G G T T T C C T G A C G G G T G G
SEQ. ID. NO. 42 A C A A C G C A A A A G G G T T G A A A G C C T T

SEQ. ID. NO. 44 G G A C C T C C C A G C T C T G G A C G G A G C C
SEQ. ID. NO. 42 C T A C G A T G C A A T A A A A T A C G G G C C G

SEQ. ID. NO. 44 C G G G T G G A T T T C C G G T G T G A C C C C G
SEQ. ID. NO. 42 A A C C A C T T G A T G G T G T T T G G A G G C G

SEQ. ID. NO. 44 A C T T C C A T C T G G T G G G C A G C T C C C G
SEQ. ID. NO. 42 T C T G T C C A T C C G T C A C A T C C A T C A T

SEQ. ID. NO. 44 G A G C A T C T G T A G T C A G G G C C A G T G G
SEQ. ID. NO. 42 T G C A G A G T C C C T C C A A G G C T G G A A T

SEQ. ID. NO. 44 A G C A C C C C C A A G C C C C A C T G C C A G G
SEQ. ID. NO. 42 C T G G T G C A G C T T T C T T T T G C T G C A A

SEQ. ID. NO. 44 T G A A T C G A A C G C C A C A C T C A G A A C G
SEQ. ID. NO. 42 C C A C G C C T G T T C T A G C C G A T A A G A A

SEQ. ID. NO. 44 G C G C G C A G T G T A C A T C G G G G C A C T G
SEQ. ID. NO. 42 A A A A T A C C C T T A T T T C T T T C G G A C C

SEQ. ID. NO. 44 T T T C C C A T G A G C G G G G G C T G G C C A G
SEQ. ID. NO. 42 G T C C C A T C A G A C A A T G C G G T G A A T C

SEQ. ID. NO. 44 G G G G C C A G G C C T G C C A G C C C G C G G T
SEQ. ID. NO. 42 C A G C C A T T C T G A A G T T G C T C A A G C A

SEQ. ID. NO. 44 G G A G A T G G C G C T G G A G G A C G T G A A T
SEQ. ID. NO. 42 C T A C C A G T G G A A G C G C G T G G G C A C G

SEQ. ID. NO. 44 A G C C G C A G G G A C A T C C T G C C G G A C T
SEQ. ID. NO. 42 C T G A C G C A A G A C G T T C A G A G G T T C T

Figure 13b

SEQ. ID. NO. 44 A T G A G C T C A A G C T C A T C C A C C A C G A
SEQ. ID. NO. 42 C T G A G G T G C G G A A T G A C C T G A C T G G

SEQ. ID. NO. 44 C A G C A A G T G T G A T C C A G G C C A A G C C
SEQ. ID. NO. 42 A G T T C T G T A T G G C G A G G A C A T T G A G

SEQ. ID. NO. 44 A C C A A G T A C C T A T A T G A G C T G C T C T
SEQ. ID. NO. 42 A T T T C A G A C A C C G A G A G C T T C T C C A

SEQ. ID. NO. 44 A C A A C G A C C C T A T C A A G A T C A T C C T
SEQ. ID. NO. 42 A C G A T C C C T G T A C C A G T G T C A A A A A

SEQ. ID. NO. 44 T A T G C C T G G C T G C A G C T C T G T C T C C
SEQ. ID. NO. 42 G C T G A A G G G G A A T G A T G T G C G G A T C

SEQ. ID. NO. 44 A C G C T G G T G G C T G A G G C T G C T A G G A
SEQ. ID. NO. 42 A T C C T T G G C C A G T T T G A C C A G A A T A

SEQ. ID. NO. 44 T G T G G A A C C T C A T T G T G C T T T C C T A
SEQ. ID. NO. 42 T G G C A G C A A A A G T G T T C T G T T G T G C

SEQ. ID. NO. 44 T G G C T C C A G C T C A C C A G C C C T G T C A
SEQ. ID. NO. 42 A T A C G A G G A G A A C A T G T A T G G T A G T

SEQ. ID. NO. 44 A A C C G G C A G C G T T T C C C C A C T T T C T
SEQ. ID. NO. 42 A A A T A T C A G T G G A T C A T T C C G G G C T

SEQ. ID. NO. 44 T C C G A A C G C A C C C A T C A G C C A C A C T
SEQ. ID. NO. 42 G G T A C G A G C C T T C T T G G T G G G A G C A

SEQ. ID. NO. 44 C C A C A A C C C T A C C C G C G T G A A A C T C
SEQ. ID. NO. 42 G G T G C A C A C G G A A G C C A A C T C A T C C

SEQ. ID. NO. 44 T T T G A A A A G T G G G G C T G G A A G A A G A
SEQ. ID. NO. 42 C G C T G C C T C C G G A A G A A T C T G C T T G

SEQ. ID. NO. 44 T T G C T A C C A T C C A G C A G A C C A C T G A
SEQ. ID. NO. 42 C T G C C A T G G A G G G C T A C A T T G G C G T

Figure 13c

SEQ. ID. NO. 44 GGTCTTCTCACTTCGACTCTGGACGAC
SEQ. ID. NO. 42 GGATTTTCGAGCCCCCTGAGCTCCAAG

SEQ. ID. NO. 44 CTGGAGGAACGAGTGAAGGAGGCTG
SEQ. ID. NO. 42 CAGATCAAGACCATCTCAGGAAAGA

SEQ. ID. NO. 44 GAATTGAGATTACTTTCCGCCAGAG
SEQ. ID. NO. 42 CTCCACAGCAGTATGAGAGAGAGTA

SEQ. ID. NO. 44 TTTCTTCTCAGATCCAGCTGTGCCC
SEQ. ID. NO. 42 CAACAACAAGCGGTCAGGCGTGGGG

SEQ. ID. NO. 44 GTCAAAAACCTGAAGCGCCAGGATG
SEQ. ID. NO. 42 CCCAGCAAGTTCCACGGGTACGCCCT

SEQ. ID. NO. 44 CCCGAATCATCTGTTGGGACTTTTCTA
SEQ. ID. NO. 42 ACGATGGCATCTGGGGTCATCGCCAA

SEQ. ID. NO. 44 TGAGACTGAAGCCCCGGAAAGTTTTT
SEQ. ID. NO. 42 GACACTGCAGAGGGCCATGGAGACA

SEQ. ID. NO. 44 TGTGAGGTGTACAAGGAGCGTCTCT
SEQ. ID. NO. 42 CTGCATGCCAGCAGCCGGGCACCCAGC

SEQ. ID. NO. 44 TTGGGAAGAAGTACGTCTGGTTTCCT
SEQ. ID. NO. 42 GGATCCAGGACTTCAACTACACGGA

SEQ. ID. NO. 44 CATTGGGTGGTATGCTGACAATTGG
SEQ. ID. NO. 42 CCACACGCTGGGGCAGGATCATCCTC

SEQ. ID. NO. 44 TTCAAGATCTACGACCCTTCTATCA
SEQ. ID. NO. 42 AATGCCATGAACGAGACCAACTTCT

SEQ. ID. NO. 44 ACTGCACAGTGGATGAGATGACTGA
SEQ. ID. NO. 42 TCGGGGTCAACGGGTCAAGTTGTATT

SEQ. ID. NO. 44 GGCGGTGGAGGGCCACATCACAACT
SEQ. ID. NO. 42 CCGGAATGGGGAGAGAAATGGGGACC

Figure 13d

SEQ. ID. NO. 44 G A G A T T G T C A T G C T G A A T C C T G C C A
SEQ. ID. NO. 42 A T T A A A T T T A C T C A A T T T C A A G A C A

SEQ. ID. NO. 44 A T A C C C G C A G C A T T T C C A A C A T G A C
SEQ. ID. NO. 42 G C A G G G A G G T G A A G G T G G G A G A G T A

SEQ. ID. NO. 44 A T C C C A G G A A T T T G T G G A G A A A C T A
SEQ. ID. NO. 42 C A A C G C T G T G G C C G A C A C A C T G G A G

SEQ. ID. NO. 44 A C C A A G C G A C T G A A A A G A C A C C C T G
SEQ. ID. NO. 42 A T C A T C A A T G A C A C C A T C A G G T T C C

SEQ. ID. NO. 44 A G G A G A C A G G A G G C T T C C A G G A G G C
SEQ. ID. NO. 42 A A G G A T C C G A A C C A C C A A A A G A C A A

SEQ. ID. NO. 44 A C C G C T G G C C T A T G A T G C C A T C T G G
SEQ. ID. NO. 42 G A C C A T C A T C C T G G A G C A G C T G C G G

SEQ. ID. NO. 44 G C C T T G G C A C T G G C C C T G A A C A A G A
SEQ. ID. NO. 42 A A G A T C T C C C T A C C T C T C T A C A G C A

SEQ. ID. NO. 44 C A T C T G G A G G A G G C G G C C G T T C T G G
SEQ. ID. NO. 42 T C C T C T C T G C C C T C A C C A T C C T C G G

SEQ. ID. NO. 44 T G T G C G C C T G G A G G A C T T C A A C T A C
SEQ. ID. NO. 42 G A T G A T C A T G G C C A G T G C T T T T C T C

SEQ. ID. NO. 44 A A C A A C C A G A C C A T T A C C G A C C A A A
SEQ. ID. NO. 42 T T C T T C A A C A T C A A G A A C C G G A A T C

SEQ. ID. NO. 44 T C T A C C G G G C A A T G A A C T C T T C G T C
SEQ. ID. NO. 42 A G A A G C T C A T A A A G A T G T C G A G T C C

SEQ. ID. NO. 44 C T T T G A G G G T G T C T C T G G C C A T G T G
SEQ. ID. NO. 42 A T A C A T G A A C A A C C T T A T C A T C C T T

SEQ. ID. NO. 44 G T G T T T G A T G C C A G C G G C T C T C G G A
SEQ. ID. NO. 42 G G A G G G A T G C T C T C C T A T G C T T C C A

Figure 13e

SEQ. ID. NO. 44 TGGCATGGACGCTTATCGAGCAGCT
SEQ. ID. NO. 42 TATTTCTCTTTTGGCCTTGATGGATC

SEQ. ID. NO. 44 TCAGGGTGGCAGCTACAAGAAGATT
SEQ. ID. NO. 42 CTTTGTCTCTGTGAAAAGACCTTTTGA

SEQ. ID. NO. 44 GGCTACTATGACAGCACCAAGGATG
SEQ. ID. NO. 42 ACACTTTGCAACCGTCAGGACCTTGA

SEQ. ID. NO. 44 ATCTTTTCCTGGTCCAAAACAGATAA
SEQ. ID. NO. 42 TTCTCACCGTGGGCTACACGACCGC

SEQ. ID. NO. 44 ATGGATTGGAGGGTCCCCCCCAGCT
SEQ. ID. NO. 42 TTTTGGGGGCCATGTTTGTCAAAGACC

SEQ. ID. NO. 44 GACCAGACCCTGGTTCATCAAGACAT
SEQ. ID. NO. 42 TGGAGAGTCCACGCCATCTTCAAAA

SEQ. ID. NO. 44 TCCGCTTTCCTGTTCACAGAAACTCTT
SEQ. ID. NO. 42 ATGTGAAAATGAAGAAGAAGATCAT

SEQ. ID. NO. 44 TATCTCCGTCTCAGTTCTCTCCAGC
SEQ. ID. NO. 42 CAAGGACCAGAAACTGCTTGTGATC

SEQ. ID. NO. 44 CTGGGCATTGTCCTAGCTGTTGTCT
SEQ. ID. NO. 42 GTGGGGGGGCATGCTGCTGATCGACC

SEQ. ID. NO. 44 GTCTGTCCTTTAACATCTACAACCTC
SEQ. ID. NO. 42 TGTGTATCCTGATCTGCTGGCAGGC

SEQ. ID. NO. 44 ACATGTCCGTTATATCCAGAACTCA
SEQ. ID. NO. 42 TGTGGACCCCCCTGCGAAGGACAGTG

SEQ. ID. NO. 44 CAGCCCAACCTGAACAACCTGACTG
SEQ. ID. NO. 42 GAGAAGTACAGCATGGAGCCGGACC

SEQ. ID. NO. 44 CTGTGGGGCTGCTCACTGGCTTTAGC
SEQ. ID. NO. 42 CAGCAGGACGGGATATCTCCATCCG

Figure 13f

SEQ. ID. NO. 44 TGCTGTCTTCCCCCTGGGGCTCGAT
SEQ. ID. NO. 42 CCTCTCTCTGGAGCACTGTGAGAAC

SEQ. ID. NO. 44 GGTTACCA CATTGGGAGGAACCA GT
SEQ. ID. NO. 42 ACCCATATGACCATCTGGCTTGGCA

SEQ. ID. NO. 44 TTCCTTTCGTCTGCCAGGCCCGCCT
SEQ. ID. NO. 42 TCGTCTATGCCTACAAGGGACTTCT

SEQ. ID. NO. 44 CTGGCTCCTGGGGCCTGGGGCTTTAGT
SEQ. ID. NO. 42 CATGTTGTTTCGGTTGTTTCTTAGCT

SEQ. ID. NO. 44 CTGGGGCTACGGTTCCATGTTTCAACCA
SEQ. ID. NO. 42 TGGGAGACCCGCAACGTCAGCATCC

SEQ. ID. NO. 44 AGATTTGGTGGGTCCACACGGTCTT
SEQ. ID. NO. 42 CCGCACTCAACGACAGCAAGTACAT

SEQ. ID. NO. 44 CACAAAGAAGGAAGAAAAGAAGGAG
SEQ. ID. NO. 42 CGGGATGAGTGCTACAACGTGGGG

SEQ. ID. NO. 44 TGGAGGAAGACTCTGGAACCCCTGGA
SEQ. ID. NO. 42 ATCATGTGCATCATCGGGGGCCGCTG

SEQ. ID. NO. 44 AGCTGTATGCCACAGTGGGGCCTGCT
SEQ. ID. NO. 42 TCTCCTTCTCTGACCCCGGGACCAAGCC

SEQ. ID. NO. 44 GGTGGGGCATGGATGTCCTCACTCTC
SEQ. ID. NO. 42 CAATGTGCAGTTCTGCATCGTGGCT

SEQ. ID. NO. 44 GCCATCTGGCAGATCGTGGACCCCTC
SEQ. ID. NO. 42 CTGGTCAATCATCTTCTGCAGCACCA

SEQ. ID. NO. 44 TGCACCGGACCAATTGAGACATTTGC
SEQ. ID. NO. 42 TCACCCCTCTGCCTGGTATTCTGTGCC

SEQ. ID. NO. 44 CAAGGAGGAACCTAAGGAAGATATT
SEQ. ID. NO. 42 GAAGCTCATCACCCCTGAGAACAAAC

Figure 13g

SEQ. ID. NO. 44 G A C G T C T C T A T T C T G C C C C A G C T G G
 SEQ. ID. NO. 42 C C A G A T G C A G C A A C G C A G A A C A G G C

SEQ. ID. NO. 44 A G C A T T G C A G C T C C A G G A A G A T G A A
 SEQ. ID. NO. 42 G A T T C C A G T T C A C T C A G A A T C A G A A

SEQ. ID. NO. 44 T A C A T G G C T T G G C A T T T T C T A T G G T
 SEQ. ID. NO. 42 G A A A G A A G A T T C T A A A A C G T C C A C C

SEQ. ID. NO. 44 T A C A A G G G G C T G C T G C T G C T G C T G G
 SEQ. ID. NO. 42 T C G G T C A C C A G T G T G A A C C A A G C C A

SEQ. ID. NO. 44 G A A T C T T C C T T G C T T A T G A G A C C A A
 SEQ. ID. NO. 42 G C A C A T C C C G C C T G G A G G G C C T A C A

SEQ. ID. NO. 44 G A G T G T G T C C A C T G A G A A G A T C A A T
 SEQ. ID. NO. 42 G T C A G A A A A C C A T C G C C T G C G A A T G

SEQ. ID. NO. 44 G A T C A C C G G G C T G T G G G C A T G G C T A
 SEQ. ID. NO. 42 A A G A T C A C A G A G C T G G A T A A A G A C T

SEQ. ID. NO. 44 T C T A C A A T G T G G C A G T C C T G T G C C T
 SEQ. ID. NO. 42 T G G A A G A G G T C A C C A T G C A G C T G C A

SEQ. ID. NO. 44 C A T C A C T G C T C C T G T C A C C A T G A T T
 SEQ. ID. NO. 42 G G A C A C A C C A G A A A A G A C C A C C T A C

SEQ. ID. NO. 44 C T G T C C A G C C A G C A G G A T G C A G C C T
 SEQ. ID. NO. 42 A T T A A A C A G A A C C A C T A C C A A G A G C

SEQ. ID. NO. 44 T T G C C T T T G C C T C T C T T G C C A T A G T
 SEQ. ID. NO. 42 T C A A T G A C A T C C T C A A C C T G G G A A A

SEQ. ID. NO. 44 T T T C T C C T C C T A T A T C A C T C T T G T T
 SEQ. ID. NO. 42 C T T C A C T G A G A G C A C A G A T G G A G G A

SEQ. ID. NO. 44 G T G C T C T T T G T G C C C A A G A T G C G C A
 SEQ. ID. NO. 42 A A G G C C A T T T T T A A A A A A T C A C C T C G

Figure 13h

SEQ. ID. NO. 44 GGCTGATCACCCGAGGGGAATGGCA
 SEQ. ID. NO. 42 ATCAAAATCCCCAGCTACAGTGGAA

SEQ. ID. NO. 44 GTCGGAGGCGCAGGACACCATGAAG
 SEQ. ID. NO. 42 CACAACAGAGCCCTCTCGAACATGTC

SEQ. ID. NO. 44 ACAGGGTTCATCGACCAACAACAACG
 SEQ. ID. NO. 42 AAAGATCCTATAGAAGATATAAACT

SEQ. ID. NO. 44 AGGAGGAGAAGTCCCCGGCTGTTGGA
 SEQ. ID. NO. 42 CTC CAGAACACATCCAGCGTCGGCT

SEQ. ID. NO. 44 GAAGGAGAACCGTGAACTGGAAAAG
 SEQ. ID. NO. 42 GTCCCTCCAGCTCCCCCATCCTCCAC

SEQ. ID. NO. 44 ATCATTTGCTGAGAAAGAGGAGCGTG
 SEQ. ID. NO. 42 CACGCCCTACCTCCCATCCATCGGAG

SEQ. ID. NO. 44 TCTCTGAACCTGCGCCATCAACTCCA
 SEQ. ID. NO. 42 GCGTGGAACGCCAGCTGTGTCTAGCCC

SEQ. ID. NO. 44 GTCTCGGCAGCAGCTCCGCTCCCCGG
 SEQ. ID. NO. 42 CTGCGTCAAGCCCCACCGCCAGCCCC

SEQ. ID. NO. 44 CGCCACCCACCGACACCCCCCAGAAC
 SEQ. ID. NO. 42 CGCCACAGACATGTGCCACCCCTCCT

SEQ. ID. NO. 44 CCTCTGGGGGGCCTGCCCAAGGGGACC
 SEQ. ID. NO. 42 TCCGAGTCAATGGTCTCGGGGCCTGGC

SEQ. ID. NO. 44 CCTTGAGCCCCCGACCGGCTTAGC
 SEQ. ID. NO. 42 GGCCGCCCATGACTCTGGAGTCCATC

SEQ. ID. NO. 44 TGTGATGGGAGTCGAGTGCAATTTGC
 SEQ. ID. NO. 42 ATGGCGTGCTGCCCTGAGCGAGGAGG

SEQ. ID. NO. 44 TTTATAAGGCGGCCCGCCATGACTCT
 SEQ. ID. NO. 42 CCAAGGAAGCCCGGCGGATCAACGA

Figure 13i

SEQ. ID. NO. 44 G G A G T C C A T C A T G G C G T G C T G C C T G
 SEQ. ID. NO. 42 C G A G A T C G A G C G G C A G C T C C G C A G G

SEQ. ID. NO. 44 A G C G A G G A G G C C A A G G A A G C C C G G C
 SEQ. ID. NO. 42 G A C A A G C G G G A C G C C C G C C G G G A G C

SEQ. ID. NO. 44 G G A T C A A C G A C G A G A T C G A G C G G C A
 SEQ. ID. NO. 42 T C A A G C T G C T G C T G C T C G G G A C A G G

SEQ. ID. NO. 44 G C T C C G C A G G G A C A A G C G G G A C G C C
 SEQ. ID. NO. 42 A G A G A G T G G C A A G A G T A C G T T T A T C

SEQ. ID. NO. 44 C G C C G G G A G C T C A A G C T G C T G C T G C
 SEQ. ID. NO. 42 A A G C A G A T G A G A A T C A T C C A T G G G T

SEQ. ID. NO. 44 T C G G G A C A G G A G A G A G T G G C A A G A G
 SEQ. ID. NO. 42 C A G G A T A C T C T G A T G A A G A T A A A A G

SEQ. ID. NO. 44 T A C G T T T A T C A A G C A G A T G A G A A T C
 SEQ. ID. NO. 42 G G G C T T C A C C A A G C T G G T G T A T C A G

SEQ. ID. NO. 44 A T C C A T G G G T C A G G A T A C T C T G A T G
 SEQ. ID. NO. 42 A A C A T C T T C A C G G C C A T G C A G G C C A

SEQ. ID. NO. 44 A A G A T A A A A G G G G C T T C A C C A A G C T
 SEQ. ID. NO. 42 T G A T C A G A G C C A T G G A C A C A C T C A A

SEQ. ID. NO. 44 G G T G T A T C A G A A C A T C T T C A C G G C C
 SEQ. ID. NO. 42 G A T C C C A T A C A A G T A T G A G C A C A A T

SEQ. ID. NO. 44 A T G C A G G C C A T G A T C A G A G C C A T G G
 SEQ. ID. NO. 42 A A G G C T C A T G C A C A A T T A G T T C G A G

SEQ. ID. NO. 44 A C A C A C T C A A G A T C C C A T A C A A G T A
 SEQ. ID. NO. 42 A A G T T G A T G T G G A G A A G G T G T C T G C

SEQ. ID. NO. 44 T G A G C A C A A T A A G G C T C A T G C A C A A
 SEQ. ID. NO. 42 T T T T G A G A A T C C A T A T G T A G A T G C A

Figure 13j

SEQ. ID. NO. 44 T T A G T T C G A G A A G T T G A T G T G G A G A
SEQ. ID. NO. 42 A T A A A G A G T T T A T G G A A T G A T C C T G

SEQ. ID. NO. 44 A G G T G T C T G C T T T T G A G A A T C C A T A
SEQ. ID. NO. 42 G A A T C C A G G A A T G C T A T G A T A G A C G

SEQ. ID. NO. 44 T G T A G A T G C A A T A A A G A G T T T A T G G
SEQ. ID. NO. 42 A C G A G A A T A T C A A T T A T C T G A C T C T

SEQ. ID. NO. 44 A A T G A T C C T G G A A T C C A G G A A T G C T
SEQ. ID. NO. 42 A C C A A A T A C T A T C T T A A T G A C T T G G

SEQ. ID. NO. 44 A T G A T A G A C G A C G A G A A T A T C A A T T
SEQ. ID. NO. 42 A C C G C G T A G C T G A C C C T G C C T A C C T

SEQ. ID. NO. 44 A T C T G A C T C T A C C A A A T A C T A T C T T
SEQ. ID. NO. 42 G C C T A C G C A A C A A G A T G T G C T T A G A

SEQ. ID. NO. 44 A A T G A C T T G G A C C G C G T A G C T G A C C
SEQ. ID. NO. 42 G T T C G A G T C C C C A C C A C A G G G A T C A

SEQ. ID. NO. 44 C T G C C T A C C T G C C T A C G C A A C A A G A
SEQ. ID. NO. 42 T C G A A T A C C C C T T T G A C T T A C A A A G

SEQ. ID. NO. 44 T G T G C T T A G A G T T C G A G T C C C C A C C
SEQ. ID. NO. 42 T G T C A T T T T T C A G A A T G G T C G A T G T A

SEQ. ID. NO. 44 A C A G G G A T C A T C G A A T A C C C C T T T G
SEQ. ID. NO. 42 G G G G G C C A A A G G T C A G A G A G A A G A A

SEQ. ID. NO. 44 A C T T A C A A A G T G T C A T T T T T C A G A A T
SEQ. ID. NO. 42 A A T G G A T A C A C T G C T T T T G A A A A T G T

SEQ. ID. NO. 44 G G T C G A T G T A G G G G G C C A A A G G T C A
SEQ. ID. NO. 42 C A C C T C T A T C A T G T T T C T A G T A G C G

SEQ. ID. NO. 44 G A G A G A A G A A A A T G G A T A C A C T G C T
SEQ. ID. NO. 42 C T T A G T G A A T A T G A T C A A G T T C T G G

Figure 13k

SEQ. ID. NO. 44 TTGAAAATGTCACCTCTATCATGTT
SEQ. ID. NO. 42 TGGAGTCAGACAAATGAGAACCGAAAT

SEQ. ID. NO. 44 TCTAGTAGCGCTTAGTGAAATATGAT
SEQ. ID. NO. 42 GGAGGAAAGCAAGGCTCTCTTTAGA

SEQ. ID. NO. 44 CAAGTTCTCTCGTGGAGTCAGACAAATG
SEQ. ID. NO. 42 ACAATTATCACATACCCCTGGTTCC

SEQ. ID. NO. 44 AGAACCGAAATGGAGGAAAGCAAGGC
SEQ. ID. NO. 42 AGAACTCCTCGGTTATTCTGTTCCTT

SEQ. ID. NO. 44 TCTCTTTAGAACAAATTATCACATAC
SEQ. ID. NO. 42 AAACAAGAAAGATCTTCTAGAGGAG

SEQ. ID. NO. 44 CCTGGTTTCCAGAACTCCTCGGTTA
SEQ. ID. NO. 42 AAAATCATGTATTCCCATCTAGTCG

SEQ. ID. NO. 44 TTCTGTTCCTTAAACAAGAAAGATCT
SEQ. ID. NO. 42 ACTACTTCCCAAGAAATATGATGGACC

SEQ. ID. NO. 44 TCTAGAGGAGAAATCATGTATTCC
SEQ. ID. NO. 42 CCAGAGAGATGCCCAAGGCAGCCCGA

SEQ. ID. NO. 44 CATCTAGTCGACTACTTCCCAAGAAAT
SEQ. ID. NO. 42 GAATTCAATTCTGAAGATGTTCTGTGG

SEQ. ID. NO. 44 ATGATGGACCCCAAGAGAGATGCCCA
SEQ. ID. NO. 42 ACCTGAACCCAGACAGTGACAAAAT

SEQ. ID. NO. 44 GGCAGCCCGAGAAATTCATTCTGAAG
SEQ. ID. NO. 42 TAACTACTCCCACTTCACTGTGCGCC

SEQ. ID. NO. 44 ATGTTCTGTGGACCTGAACCCAGACA
SEQ. ID. NO. 42 ACAGACACCGAGAAATATCCGCTTTG

SEQ. ID. NO. 44 GTGACAAAAATTATCTACTCCCACTT
SEQ. ID. NO. 42 TCTTTGCTGCCGTCAAGGACACCAAT

Figure 13L

SEQ. ID. NO. 44 C A C G T G C G C C A C A G A C A C C G A G A A T
SEQ. ID. NO. 42 C C T C C A G T T G A A C C T G A A G G G C T G C

SEQ. ID. NO. 44 A T C C G C T T T G T C T T T G C T G C C G T C A
SEQ. ID. NO. 42 G G T C T G T A C

SEQ. ID. NO. 44 A G G A C A C C A T C C T C C A G T T G A A C C T
SEQ. ID. NO. 42

SEQ. ID. NO. 44 G A A G G G C T G C G G T C T G T A C
SEQ. ID. NO. 42

Figure 13M

ClustalW Formatted Alignments

SEQ. ID. NO. 45 M L L L L L L A P L F L R P P G A G G A Q T P N A
SEQ. ID. NO. 43 M A S P R S S G Q P G P P P P P P P P A R L L L

SEQ. ID. NO. 45 T S E G C Q I I H P P W E G G I R Y R G L T R D Q
SEQ. ID. NO. 43 L L L L P L L L P L A P G A W G W A R G A P R P P

SEQ. ID. NO. 45 V K A I N F L P V D Y E I E Y V C R G E R E V V G
SEQ. ID. NO. 43 P S S P P L S I M G L M P L T K E V A K G S I G R

SEQ. ID. NO. 45 P K V R K C L A N G S W T D M D T P S R C V R I C
SEQ. ID. NO. 43 G V L P A V E L A I E Q I R N E S L L R P Y F L D

SEQ. ID. NO. 45 S K S Y L T L E N G K V F L T G G D L P A L D G A
SEQ. ID. NO. 43 L R L Y D T E C D N A K G L K A F Y D A I K Y G P

SEQ. ID. NO. 45 R V D F R C D P D F H L V G S S R S I C S Q G Q W
SEQ. ID. NO. 43 N H L M V F G G V C P S V T S I I A E S L Q G W N

SEQ. ID. NO. 45 S T P K P H C Q V N R T P H S E R R A V Y I G A L
SEQ. ID. NO. 43 L V Q L S F A A T T P V L A D K K K Y P Y F F R T

SEQ. ID. NO. 45 F P M S G G W P G G Q A C Q P A V E M A L E D V N
SEQ. ID. NO. 43 V P S D N A V N P A I L K L L K H Y Q W K R V G T

SEQ. ID. NO. 45 S R R D I L P D Y E L K L I H H D S K C D P G Q A
SEQ. ID. NO. 43 L T Q D V Q R F S E V R N D L T G V L Y G E D I E

SEQ. ID. NO. 45 T K Y L Y E L L Y N D P I K I I L M P G C S S V S
SEQ. ID. NO. 43 I S D T E S F S N D P C T S V K K L K G N D V R I

SEQ. ID. NO. 45 T L V A E A A R M W N L I V L S Y G S S S P A L S
SEQ. ID. NO. 43 I L G Q F D Q N M A A K V F C C A Y E E N M Y G S

SEQ. ID. NO. 45 N R Q R F P T F F R T H P S A T L H N P T R V K L
SEQ. ID. NO. 43 K Y Q W I I P G W Y E P S W W E Q V H T E A N S S

Figure 14a

SEQ. ID. NO. 45 FEK WGWKKIATIQQTTTEVFTSTLDD
SEQ. ID. NO. 43 RCLRKNNLLAAMEGYIGVDFEPLSSK

SEQ. ID. NO. 45 LEERVKEAGIEITFRQSFFSDPAVP
SEQ. ID. NO. 43 QIKTISGKTPQQYEREYNNKRSGVG

SEQ. ID. NO. 45 VKNLKRQDARIIVGLFYETEARKV F
SEQ. ID. NO. 43 PSKFHGYAYDGIWVIAKTLQRAMET

SEQ. ID. NO. 45 CEVYKERLFGKKYVWFLIGWYADNW
SEQ. ID. NO. 43 LHASSRHQRIQDFNYTDHTLGRIL

SEQ. ID. NO. 45 FKIYDPSINCTVDEMTEAVEGHITT
SEQ. ID. NO. 43 NAMNETNPFVGVTGQVVFRNGERMGT

SEQ. ID. NO. 45 EIVMLNPANTRISISNMTSQEFVEKL
SEQ. ID. NO. 43 IKFTQFQDSREVKVGEYNAVADTLE

SEQ. ID. NO. 45 TKRLKRHPREETGG - FQEAPLAYDAI
SEQ. ID. NO. 43 IINDTIRFQGSEPPKDKTIILEQLR

SEQ. ID. NO. 45 WALALALNKTSGGGGRSGVRLEDNFN
SEQ. ID. NO. 43 KISLPLYSILSALTILGMIMASAF L

SEQ. ID. NO. 45 YNNQTITDQIYRAMNSSSSFEGVSGH
SEQ. ID. NO. 43 FFNIKNRNQKLIKMS SPYMNLIIL

SEQ. ID. NO. 45 VVFDASGSRMAWTLIEQLQGGSYKK
SEQ. ID. NO. 43 GGMLSYASIFLFGLDGSFVSEKTFE

SEQ. ID. NO. 45 IGY YDSTKDDL SWSKTDKWIGGSPP
SEQ. ID. NO. 43 TLCTVRTWILT VGYTTAFGAMFAKT

SEQ. ID. NO. 45 ADQTLVIKTFRFLSQKLFISVSVLS
SEQ. ID. NO. 43 WRVHAIFKNVKMKKKI IKDQKLLVI

SEQ. ID. NO. 45 SLGIVLAVVCLSFNIYN SHVRYIQN
SEQ. ID. NO. 43 VGGMLLIDLCILICWQAVDPLRRTV

Figure 14b

SEQ. ID. NO. 45 S Q P N L N N L T A V G C S L A L A A V F P L G L
SEQ. ID. NO. 43 E K Y S M E P D P A G R D I S I R P L L E H C E N

SEQ. ID. NO. 45 D G Y H I G R N Q F P F V C Q A R L W L L G L G F
SEQ. ID. NO. 43 T H M T I W L G I V Y A Y K G L L M L F G C F L A

SEQ. ID. NO. 45 S L G Y G S M F T K I W W V H T V F T K K E E K K
SEQ. ID. NO. 43 W E T R N V S I P A L N D S K Y I G M S V Y N V G

SEQ. ID. NO. 45 E W R K T L E P W K L Y A T V G L L V G M D V L T
SEQ. ID. NO. 43 I M C I I G A A V S F L T R D Q P N V Q F C I V A

SEQ. ID. NO. 45 L A I W Q I V D P L H R T I E T F A K E E P K E D
SEQ. ID. NO. 43 L V I I F C S T I T L C L V F V P K L I T L R T N

SEQ. ID. NO. 45 I D V S I L P Q L E H C S S R K M N T W L G I F Y
SEQ. ID. NO. 43 P D A A T Q N R R F Q F T Q N Q K K E D S K T S T

SEQ. ID. NO. 45 G Y K G L L L L L G I F L A Y E T K S V S T E K I
SEQ. ID. NO. 43 S V T S V N Q A S T S R L E G L Q S E N H R L R M

SEQ. ID. NO. 45 N D H R A V G M A I Y N V A V L C L I T A P V T M
SEQ. ID. NO. 43 K I T E L D K D L E E V T M Q L Q D T P E K T T Y

SEQ. ID. NO. 45 I L S S Q Q D A A F A F A S L A I V F S S Y I T L
SEQ. ID. NO. 43 I K Q N H Y Q E L N D I L N L G N F T E S T D G G

SEQ. ID. NO. 45 V V L F V P K M R R L I T R G E W Q S E A Q D T M
SEQ. ID. NO. 43 K A I L K N H L D Q N P Q L Q W N T T E P S R T C

SEQ. ID. NO. 45 K T G S S T N N N E E E K S R L L E K E N R E L E
SEQ. ID. NO. 43 K D P I E D I N S P E H I Q R R L S L Q L P I L H

SEQ. ID. NO. 45 K I I A E K E E R V S E L R H Q L Q S R Q Q L R S
SEQ. ID. NO. 43 H A Y L P S I G G V D A S C V S P C V S P T A S P

SEQ. ID. NO. 45 R R H P P T P P E P S G G L P R G P P E P P D R L
SEQ. ID. NO. 43 R H R H V P P S F R V M V S G L A A A M T L E S I

Figure 14c

SEQ. ID. NO. 45 SCDGSRVHLLYKAAAMTLESIMACC
SEQ. ID. NO. 43 MACCLSEEAKEARRINDEIERQLRR

SEQ. ID. NO. 45 LSEEAKEARRINDEIERQLRRDKRD
SEQ. ID. NO. 43 DKRDARRELKLLLLLGTGESGKSTFI

SEQ. ID. NO. 45 ARRELKLLLLLGTGESGKSTFIKQMR
SEQ. ID. NO. 43 KQMRIIHGSGYSDEEDKRGFTKLVYQ

SEQ. ID. NO. 45 IIHGSGYSDEEDKRGFTKLVYQNIFT
SEQ. ID. NO. 43 NIFTAMQAMIRAMD TLKIPYKYEHN

SEQ. ID. NO. 45 AMQAMIRAMD TLKIPYKYEHNKAHA
SEQ. ID. NO. 43 KAHAQLVREVDVEKVS AFENPYVDA

SEQ. ID. NO. 45 QLVREVDVEKVS AFENPYVDAIKSL
SEQ. ID. NO. 43 IKS LWN DPGIQECYDRRREYQLSDS

SEQ. ID. NO. 45 WNDPGIQECYDRRREYQLSDSTKYY
SEQ. ID. NO. 43 TKYYLNDLDRVADPAYLPTQQQDVLR

SEQ. ID. NO. 45 LNDLDRVADPAYLPTQQQDVLRVRVP
SEQ. ID. NO. 43 VRVP TTGIIEY PFDLQSVIFRMVDV

SEQ. ID. NO. 45 TTGIIEY PFDLQSVIFRMVDVGGQR
SEQ. ID. NO. 43 GGQRSE R R K W I H C F E N V T S I M F L V A

SEQ. ID. NO. 45 SE R R K W I H C F E N V T S I M F L V A L S E Y
SEQ. ID. NO. 43 LSEYDQVLVESDNENRMEESKALFR

SEQ. ID. NO. 45 DQVLVESDNENRMEESKALFR TIIT
SEQ. ID. NO. 43 TIITYPWFQNSSSVILFLNKKDLLEE

SEQ. ID. NO. 45 YPWFQNSSSVILFLNKKDLLEEKIMY
SEQ. ID. NO. 43 KIMYSHLVDFPEYDGPQRDAQAAR

SEQ. ID. NO. 45 SHLVDFPEYDGPQRDAQAAREFIL
SEQ. ID. NO. 43 EFILKMFVDLNPDS DKINYSHF TCA

Figure 14d

SEQ. ID. NO. 45 KMFVDLNPDSDKIIYSHFTCATDTE
SEQ. ID. NO. 43 TDTENIRFVF AAVKDTILQLNLKGC

SEQ. ID. NO. 45 NIRFVF AAVKDTILQLNLKGCGLY
SEQ. ID. NO. 43 GLY

Figure 14e

mGluR8//CaR*Gqi5

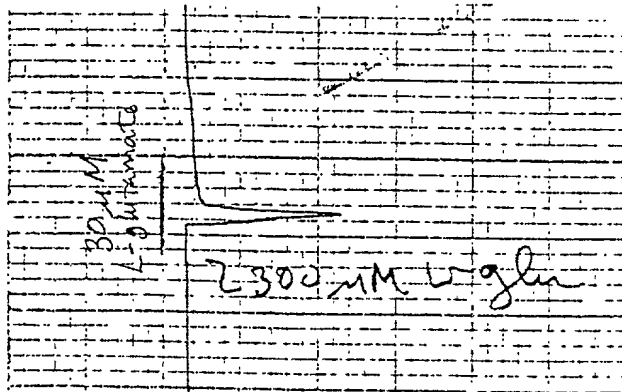
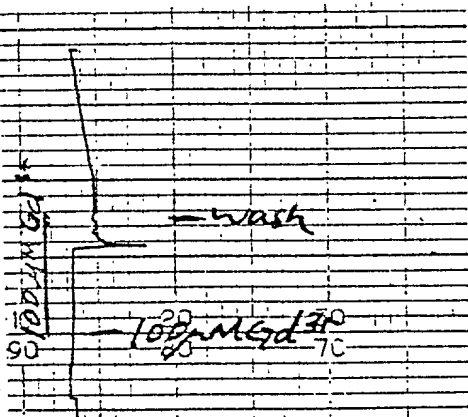


Figure 15

CaR/mGluR2*Gqi5



mGluR2//CaR*Gqi5

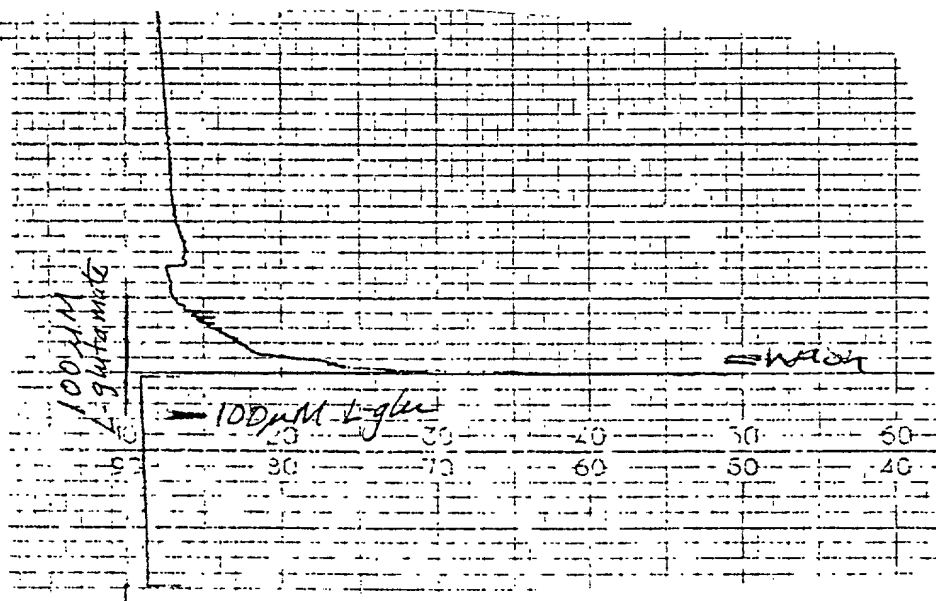


FIGURE 16A

SEQ. ID. NO. 48 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R
 SEQ. ID. NO. 49 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R
 SEQ. ID. NO. 50 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R

SEQ. ID. NO. 48 T H S Q E Y A H S I R I D G D I T L G G L F P V H G R G S E
 SEQ. ID. NO. 49 T H S Q E Y A H S I R I D G D I T L G G L F P V H G R G S E
 SEQ. ID. NO. 50 T H S Q E Y A H S I R V D G D I I L G G L F P V H A K G E R

SEQ. ID. NO. 48 G K P C G E L K K E K G I H R L E A M L F A L D R I N N D P
 SEQ. ID. NO. 49 G K P C G E L K K E K G I H R L E A M L F A L D R I N N D P
 SEQ. ID. NO. 50 G V P C G E L K K E K G I H R L E A M L Y A I D Q I N K D P

SEQ. ID. NO. 48 D L L P N I T L G A R I L D T C S R D T H A L E Q S L T F V
 SEQ. ID. NO. 49 D L L P N I T L G A R I L D T C S R D T H A L E Q S L T F V
 SEQ. ID. NO. 50 D L L S N I T L G V R I L D T C S R D T Y A L E Q S L T F V

SEQ. ID. NO. 48 Q A L I E K D G T E V R C G S G G P P I I T K P E R V V G V
 SEQ. ID. NO. 49 Q A L I E K D G T E V R C G S G G P P I I T K P E R V V G V
 SEQ. ID. NO. 50 Q A L I E K D A S D V K C A N G D P P I F T K P D K I S G V

SEQ. ID. NO. 48 I G A S G S S V S I M V A N I L R L F K I P Q I S Y A S T A
 SEQ. ID. NO. 49 I G A S G S S V S I M V A N I L R L F K I P Q I S Y A S T A
 SEQ. ID. NO. 50 I G A A A S S V S I M V A N I L R L F K I P Q I S Y A S T A

SEQ. ID. NO. 48 P D L S D N S R Y D F F S R V V P S D T Y Q A Q A M V D I V
 SEQ. ID. NO. 49 P D L S D N S R Y D F F S R V V P S D T Y Q A Q A M V D I V
 SEQ. ID. NO. 50 P E L S D N T R Y D F F S R V V P P D S Y Q A Q A M V D I V

SEQ. ID. NO. 48 R A L K W N Y V S T V A S E G S Y G E S G V E A F I Q K S R
 SEQ. ID. NO. 49 R A L K W N Y V S T V A S E G S Y G E S G V E A F I Q K S R
 SEQ. ID. NO. 50 T A L G W N Y V S T L A S E G N Y G E S G V E A F T Q I S R

SEQ. ID. NO. 48 E D G G V C I A Q S V K I P R E P K A G E F D K I I R R L L
 SEQ. ID. NO. 49 E D G G V C I A Q S V K I P R E P K A G E F D K I I R R L L
 SEQ. ID. NO. 50 E I G G V C I A Q S Q K I P R E P R P G E F E K I I K R L L

FIGURE 16B

SEQ. ID. NO. 48 E T S N A R A V I I F A N E D D I R R V L E A A R R A N Q T
 SEQ. ID. NO. 49 E T S N A R A V I I F A N E D D I R R V L E A A R R A N Q T
 SEQ. ID. NO. 50 E T P N A R A V I M F A N E D D I R R I L E A A K K L N Q S

SEQ. ID. NO. 48 G H F F W M G S D S W G S K I A P V L H L E E V A E G A V T
 SEQ. ID. NO. 49 G H F F W M G S D S W G S K I A P V L H L E E V A E G A V T
 SEQ. ID. NO. 50 G H F L W I G S D S W G S K I A P V Y Q Q E E I A E G A V T

SEQ. ID. NO. 48 I L P K R M S V R G F D R Y F S S R T L D N N R R N I W F A
 SEQ. ID. NO. 49 I L P K R M S V R G F D R Y F S S R T L D N N R R N I W F A
 SEQ. ID. NO. 50 I L P K R A S I D G F D R Y F R S R T L A N N R R N V W F A

SEQ. ID. NO. 48 E F W E D N F H C K L S R H A L K K G S H V K K C T N R E R
 SEQ. ID. NO. 49 E F W E D N F H C K L S R H A L K K G S H V K K C T N R E R
 SEQ. ID. NO. 50 E F W E E N F G C K L G S H G K R N - S H I K K C T G L E R

SEQ. ID. NO. 48 I G Q D S A Y E Q E G K V Q F V I D A V Y A M G H A L H A M
 SEQ. ID. NO. 49 I G Q D S A Y E Q E G K V Q F V I D A V Y A M G H A L H A M
 SEQ. ID. NO. 50 I A R D S S Y E Q E G K V Q F V I D A V Y S M A Y A L H N M

SEQ. ID. NO. 48 H R D L C P G R V G L C P R M D P V D G T Q L L K Y I R N V
 SEQ. ID. NO. 49 H R D L C P G R V G L C P R M D P V D G T Q L L K Y I R N V
 SEQ. ID. NO. 50 H K D L C P G Y I G L C P R M S T I D G K E L L G Y I R A V

SEQ. ID. NO. 48 N F S G I A G N P V T F N E N G D A P G R Y D I Y Q Y Q L R
 SEQ. ID. NO. 49 N F S G I A G N P V T F N E N G D A P G R Y D I Y Q Y Q L R
 SEQ. ID. NO. 50 N F N G S A G T P V T F N E N G D A P G R Y D I F Q Y Q I T

SEQ. ID. NO. 48 N D S A E Y K V I G S W T D H L H L R I E R M H W P G S G Q
 SEQ. ID. NO. 49 N D S A E Y K V I G S W T D H L H L R I E R M H W P G S G Q
 SEQ. ID. NO. 50 N K S T E Y K V I G H W T N Q L H L K V E D M Q W A H R E H

SEQ. ID. NO. 48 Q L P R S I C S L P C Q P G E R K K T V K G M P C C W H C E
 SEQ. ID. NO. 49 Q L P R S I C S L P C Q P G E R K K T V K G M P C C W H C E
 SEQ. ID. NO. 50 T H P A S V C S L P C K P G E R K K T V K G V P C C W H C E

SEQ. ID. NO. 48 P C T G Y Q Y Q V D R Y T C K T C P Y D M R P T E N R T G C
 SEQ. ID. NO. 49 P C T G Y Q Y Q V D R Y T C K T C P Y D M R P T E N R T G C
 SEQ. ID. NO. 50 R C E G Y N Y Q V D E L S C E L C P L D Q R P N M N R T G C

FIGURE 16C

SEQ. ID. NO. 48 R P I P I I K L E W G S P W A V L P L F L A V V G I A A T L
 SEQ. ID. NO. 49 R P I P I I K L E W G S P W A V L P L F L A V V G I A A T L
 SEQ. ID. NO. 50 Q L I P I I K L E W H S P W A V V P V F V A I L G I I A T T

SEQ. ID. NO. 48 F V V I T F V R Y N D T P I V K A S G R E L S Y V L L A G I
 SEQ. ID. NO. 49 F V V I T F V R Y N D T P I V K A S G R E L S Y V L L A G I
 SEQ. ID. NO. 50 F V I V T F V R Y N D T P I V R A S G R E L S Y V L L T G I

SEQ. ID. NO. 48 F L C Y A T T F L M I A E P D L G T C S L R R I F L G L G M
 SEQ. ID. NO. 49 F L C Y A T T F L M I A E P D L G T C S L R R I F L G L G M
 SEQ. ID. NO. 50 F L C Y S I T F L M I A A P D T I I C S F R R V F L G L G M

SEQ. ID. NO. 48 S I S Y A A L L T K T N R I Y R I F E Q G K R S V S A P R F
 SEQ. ID. NO. 49 S I S Y A A L L T K T N R I Y R I F E Q G K R S V S A P R F
 SEQ. ID. NO. 50 C F S Y A A L L T K T N R I H R I F E Q G K K S V T A P K F

SEQ. ID. NO. 48 I S P A S Q L A I T F S L I S L Q L L G I C V W F V V D P S
 SEQ. ID. NO. 49 I S P A S Q L A I T F S L I S L Q L L G I C V W F V V D P S
 SEQ. ID. NO. 50 I S P A S Q L V I T F S L I S V Q L L G V F V W F V V D P P

SEQ. ID. NO. 48 H S V V D F Q D Q R T L D P R F A R G V L K C D I S D L S L
 SEQ. ID. NO. 49 H S V V D F Q D Q R T L D P R F A R G V L K C D I S D L S L
 SEQ. ID. NO. 50 H I I I D Y G E Q R T L D P E K A R G V L K C D I S D L S L

SEQ. ID. NO. 48 I C L L G Y S M L L M V T C T V Y A I K T R G V P E T F N E
 SEQ. ID. NO. 49 I C L L G Y S M L L M V T C T V Y A I K T R G V P E T F N E
 SEQ. ID. NO. 50 I C S L G Y S I L L M V T C T V Y A I K T R G V P E T F N E

SEQ. ID. NO. 48 A K P I G F T M Y T T C I V W L A F I P I F F G T S Q S A D
 SEQ. ID. NO. 49 A K P I G F T M Y T T C I V W L A F I P I F F G T S Q S A D
 SEQ. ID. NO. 50 A K P I G F T M Y T T C I I W L A F I P I F F G T A Q S A E

SEQ. ID. NO. 48 K L Y I Q T T T L T V S V S L S A S V S L G M L Y M P K V Y
 SEQ. ID. NO. 49 K L Y I Q T T T L T V S V S L S A S V S L G M L Y M P K V Y
 SEQ. ID. NO. 50 K M Y I Q T T T L T V S M S L S A S V S L G M L Y M P K V Y

SEQ. ID. NO. 48 I I L F H P E Q N V P K R K R S L K A V V T A A T M S N K F
 SEQ. ID. NO. 49 I I L F H P E Q N T I E E V R C S T A A H A F K V A A R A T
 SEQ. ID. NO. 50 I I I F H P E Q N T I E E V R C S T A A H A F K V A A R A T

FIGURE 16D

SEQ. ID. NO. 48 T Q K G N F R P N G E A K S E L C E N L E A P A L A T K Q T
SEQ. ID. NO. 49 L R R S N V S R K R S S S L G G S T G S T P S S S I S S K S
SEQ. ID. NO. 50 L R R S N V S R K R S S S L G G S T G S T P S S S I S S K S

SEQ. ID. NO. 48 Y V T Y T N H A I
SEQ. ID. NO. 49 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L
SEQ. ID. NO. 50 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L

SEQ. ID. NO. 48
SEQ. ID. NO. 49 T L P Q Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S
SEQ. ID. NO. 50 T L P Q Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S

SEQ. ID. NO. 48
SEQ. ID. NO. 49 F D E P Q K N A M A H G N S T H Q N S L E A Q K S S D T L T
SEQ. ID. NO. 50 F D E P Q K N A M A H G N S T H Q N S L E A Q K S S D T L T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 R H Q P L L P L Q C G E T D L D L T V Q E T G L Q G P V G G
SEQ. ID. NO. 50 R H Q P L L P L Q C G E T D L D L T V Q E T G L Q G P V G G

SEQ. ID. NO. 48
SEQ. ID. NO. 49 D Q R P E V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 50 D Q R P E V E D P E E L S P A L V V S S S Q S F V I S G G G

SEQ. ID. NO. 48
SEQ. ID. NO. 49 S T V T E N V V N S A A A M T L E S I M A C C L S E E A K E
SEQ. ID. NO. 50 S T V T E N V V N S A A A M T L E S I M A C C L S E E A K E

SEQ. ID. NO. 48
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SEQ. ID. NO. 50 A R R I N D E I E R Q L R R D K R D A R R E L K L L L L G T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 G E S G K S T F I K Q M R I I H G S G Y S D E D K R G F T K
SEQ. ID. NO. 50 G E S G K S T F I K Q M R I I H G S G Y S D E D K R G F T K

SEQ. ID. NO. 48
SEQ. ID. NO. 49 L V Y Q N I F T A M Q A M I R A M D T L K I P Y K Y E H N K
SEQ. ID. NO. 50 L V Y Q N I F T A M Q A M I R A M D T L K I P Y K Y E H N K

FIGURE 16E

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

A H A Q L V R E V D V E K V S A F E N P Y V D A I K S L W N
A H A Q L V R E V D V E K V S A F E N P Y V D A I K S L W N

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R V
D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R V

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q
A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M
S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

F L V A L S E Y D Q V L V E S D N E N R M E E S K A L F R T
F L V A L S E Y D Q V L V E S D N E N R M E E S K A L F R T

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

I I T Y P W F Q N S S V I L F L N K K D L L E E K I M Y S H
I I T Y P W F Q N S S V I L F L N K K D L L E E K I M Y S H

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

L V D Y F P E Y D G P Q R D A Q A A R E F I L K M F V D L N
L V D Y F P E Y D G P Q R D A Q A A R E F I L K M F V D L N

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

P D S D K I I Y S H F T C A T D T E N I R F V F A A V K D T
P D S D K I I Y S H F T C A T D T E N I R F V F A A V K D T

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

I L Q L N L K D C G L F
I L Q L N L K D C G L F

SEQUENCE LISTING

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<120> G-PROTEIN FUSION RECEPTORS AND CHIMERIC
GABAB RECEPTORS

<130> 241/086-CIP

<140> TO BE ASSIGNED

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<151> 1998-04-03

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<151> 1999-04-02

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<212> PRT

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      20              25              30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
 35              40              45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
 50              55              60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
 65              70              75              80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
      85              90              95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
 100              105              110

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Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
 115 120 125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
 130 135 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
 145 150 155 160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
 165 170 175

Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
 180 185 190

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
 195 200 205

Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
 210 215 220

Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
 225 230 235 240

Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
 245 250 255

Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
 260 265 270

Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
 275 280 285

Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
 290 295 300

Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
 305 310 315 320

Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
 325 330 335

Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
 340 345 350

Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
 355 360 365

Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
 370 375 380

Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
 385 390 395 400

Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile

405 410 415
 Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
 420 425 430
 Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
 435 440 445
 Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
 450 455 460
 Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
 465 470 475 480
 Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
 485 490 495
 Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
 500 505 510
 Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
 515 520 525
 Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
 530 535 540
 Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
 545 550 555 560
 Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
 565 570 575
 Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
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 Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp
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 Thr Glu Pro Phe
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Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35 40 45
 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
 50 55 60
 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
 65 70 75 80
 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
 85 90 95
 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
 100 105 110
 Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
 115 120 125
 Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile
 130 135 140
 Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn
 145 150 155 160
 Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe
 165 170 175
 Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val
 180 185 190
 Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp
 195 200 205
 Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln
 210 215 220
 Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile
 225 230 235 240
 Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
 245 250 255
 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro
 260 265 270
 Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro
 275 280 285
 Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
 290 295 300
 Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
 305 310 315 320
 Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
 325 330 335

Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
 340 345 350
 Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
 355 360 365
 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
 370 375 380
 Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp
 385 390 395 400
 Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr
 405 410 415
 Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro
 420 425 430
 Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu
 435 440 445
 Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe
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 Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala
 465 470 475 480
 Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu
 485 490 495
 Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala
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 Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp
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 Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly
 530 535 540
 Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu
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 Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp
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Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser
      35           40           45

Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
 50           55           60

Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
65           70           75           80

Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
      85           90           95

Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
      100          105          110

Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
      115          120          125

Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
      130          135          140

Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
      145          150          155          160

Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
      165          170          175

Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
      180          185          190

Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
      195          200          205

Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
      210          215          220

Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
      225          230          235          240

Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
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Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
      260          265          270

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Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp
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 Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
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 Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
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 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
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 Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
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 385 390 395 400
 Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg
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Pro	Pro	Pro	Ser	Ser	Pro	Pro	Leu	Ser	Ile	Met	Gly	Leu	Met	Pro	Leu
50					55					60					
Thr	Lys	Glu	Val	Ala	Lys	Gly	Ser	Ile	Gly	Arg	Gly	Val	Leu	Pro	Ala
65					70					75					80
Val	Glu	Leu	Ala	Ile	Glu	Gln	Ile	Arg	Asn	Glu	Ser	Leu	Leu	Arg	Pro
				85					90					95	
Tyr	Phe	Leu	Asp	Leu	Arg	Leu	Tyr	Asp	Thr	Glu	Cys	Asp	Asn	Ala	Lys
			100					105					110		
Gly	Leu	Lys	Ala	Phe	Tyr	Asp	Ala	Ile	Lys	Tyr	Gly	Pro	Asn	His	Leu
		115					120					125			
Met	Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr	Ser	Ile	Ile	Ala	Glu
	130					135					140				
Ser	Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Thr
145					150					155					160
Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Phe	Phe	Arg	Thr	Val
				165					170					175	
Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu	Lys	Leu	Leu	Lys	His
			180					185					190		
Tyr	Gln	Trp	Lys	Arg	Val	Gly	Thr	Leu	Thr	Gln	Asp	Val	Gln	Arg	Phe
		195					200					205			
Ser	Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu	Tyr	Gly	Glu	Asp	Ile
	210					215					220				
Glu	Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp	Pro	Cys	Thr	Ser	Val
225					230					235					240
Lys	Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile	Leu	Gly	Gln	Phe	Asp
				245					250					255	
Gln	Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala	Tyr	Glu	Glu	Asn	Met
			260					265					270		
Tyr	Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly	Trp	Tyr	Glu	Pro	Ser
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Trp	Trp	Glu	Gln	Val	His	Thr	Glu	Ala	Asn	Ser	Ser	Arg	Cys	Leu	Arg
	290					295					300				
Lys	Asn	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile	Gly	Val	Asp	Phe	Glu
305					310					315					320
Pro	Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser	Gly	Lys	Thr	Pro	Gln
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Gln Tyr Glu Arg Glu Tyr Asn Asn Lys Arg Ser Gly Val Gly Pro Ser
340 345 350

Lys Phe His Gly Tyr Ala Tyr Asp Gly Ile Trp Val Ile Ala Lys Thr
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Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg
370 375 380

Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu
385 390 395 400

Asn Ala Met Asn Glu Thr Asn Phe Phe Gly Val Thr Gly Gln Val Val
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Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln
420 425 430

Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr
435 440 445

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35 40 45

Gly Gly Leu Phe Pro Val His Ala Lys Gly Glu Arg Gly Val Pro Cys
50 55 60

Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
65 70 75 80

Tyr Ala Ile Asp Gln Ile Asn Lys Asp Pro Asp Leu Leu Ser Asn Ile
85 90 95

Thr Leu Gly Val Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala
100 105 110

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

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 Asp Lys Ile Ser Gly Val Ile Gly Ala Ala Ala Ser Ser Val Ser Ile
 145 150 155 160
 Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
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 Ala Ser Thr Ala Pro Glu Leu Ser Asp Asn Thr Arg Tyr Asp Phe Phe
 180 185 190
 Ser Arg Val Val Pro Pro Asp Ser Tyr Gln Ala Gln Ala Met Val Asp
 195 200 205
 Ile Val Thr Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu
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 Gly Asn Tyr Gly Glu Ser Gly Val Glu Ala Phe Thr Gln Ile Ser Arg
 225 230 235 240
 Glu Ile Gly Gly Val Cys Ile Ala Gln Ser Gln Lys Ile Pro Arg Glu
 245 250 255
 Pro Arg Pro Gly Glu Phe Glu Lys Ile Ile Lys Arg Leu Leu Glu Thr
 260 265 270
 Pro Asn Ala Arg Ala Val Ile Met Phe Ala Asn Glu Asp Asp Ile Arg
 275 280 285
 Arg Ile Leu Glu Ala Ala Lys Lys Leu Asn Gln Ser Gly His Phe Leu
 290 295 300
 Trp Ile Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Tyr Gln
 305 310 315 320
 Gln Glu Glu Ile Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Ala
 325 330 335
 Ser Ile Asp Gly Phe Asp Arg Tyr Phe Arg Ser Arg Thr Leu Ala Asn
 340 345 350
 Asn Arg Arg Asn Val Trp Phe Ala Glu Phe Trp Glu Glu Asn Phe Gly
 355 360 365
 Cys Lys Leu Gly Ser His Gly Lys Arg Asn Ser His Ile Lys Lys Cys
 370 375 380
 Thr Gly Leu Glu Arg Ile Ala Arg Asp Ser Ser Tyr Glu Gln Glu Gly
 385 390 395 400
 Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ser Met Ala Tyr Ala Leu
 405 410 415

His Asn Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro
 420 425 430
 Arg Met Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala
 435 440 445
 Val Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Thr Phe Asn Glu Asn
 450 455 460
 Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Ile Thr Asn
 465 470 475 480
 Lys Ser Thr Glu Tyr Lys Val Ile Gly His Trp Thr Asn Gln Leu His
 485 490 495
 Leu Lys Val Glu Asp Met Gln Trp Ala His Arg Glu His Thr His Pro
 500 505 510
 Ala Ser Val Cys Ser Leu Pro Cys Lys Pro Gly Glu Arg Lys Lys Thr
 515 520 525
 Val Lys Gly Val Pro Cys Cys Trp His Cys Glu Arg Cys Glu Gly Tyr
 530 535 540
 Asn Tyr Gln Val Asp Glu Leu Ser Cys Glu Leu Cys Pro Leu Asp Gln
 545 550 555 560
 Arg Pro Asn Met Asn Arg Thr Gly Cys Gln Leu Ile Pro Ile Ile Lys
 565 570 575
 Leu Glu Trp His Ser Pro Trp
 580

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 Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Leu Cys
 35 40 45
 Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro Gln Asp Trp Thr
 50 55 60
 Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile

65	70	75	80
Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala	85	90	95
Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly Leu Asn Leu Gln	100	105	110
Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile Val Ile Cys Val	115	120	125
Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn Gln Glu Leu	130	135	140
Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly Ser Leu Met Ala	145	150	155
Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe	165	170	175
Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala	180	185	190
Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser	195	200	205
Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val	210	215	220
Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile	225	230	235
Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe	245	250	

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Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile	20	25	30	
Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser	35	40	45	
Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile	50	55	60	

Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
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 Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
 85 90 95
 Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
 100 105 110
 Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
 115 120 125
 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
 130 135 140
 His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
 145 150 155 160
 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
 165 170 175
 Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
 180 185 190
 Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 195 200 205
 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 210 215 220
 Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 225 230 235 240
 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 245 250 255
 Ile Thr Leu Val Val Leu Phe Val Pro Lys Met
 260 265

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 <211> 267
 <212> PRT
 <213> Human

<400> 8

Leu Phe Ile Ser Val Ser Val Leu Ser Ser Leu Gly Ile Val Leu Ala
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 Val Val Cys Leu Ser Phe Asn Ile Tyr Asn Ser His Val Arg Tyr Ile
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 Gln Asn Ser Gln Pro Asn Leu Asn Asn Leu Thr Ala Val Gly Cys Ser
 35 40 45

Leu Ala Leu Ala Ala Val Phe Pro Leu Gly Leu Asp Gly Tyr His Ile
 50 55 60
 Gly Arg Asn Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu
 65 70 75 80
 Gly Leu Gly Phe Ser Leu Gly Tyr Gly Ser Met Phe Thr Lys Ile Trp
 85 90 95
 Trp Val His Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg
 100 105 110
 Lys Thr Leu Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val
 115 120 125
 Gly Met Asp Val Leu Thr Leu Ala Ile Trp Gln Ile Val Asp Pro Leu
 130 135 140
 His Arg Thr Ile Glu Thr Phe Ala Lys Glu Glu Pro Lys Glu Asp Ile
 145 150 155 160
 Asp Val Ser Ile Leu Pro Gln Leu Glu His Cys Ser Ser Arg Lys Met
 165 170 175
 Asn Thr Trp Leu Gly Ile Phe Tyr Gly Tyr Lys Gly Leu Leu Leu Leu
 180 185 190
 Leu Gly Ile Phe Leu Ala Tyr Glu Thr Lys Ser Val Ser Thr Glu Lys
 195 200 205
 Ile Asn Asp His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val
 210 215 220
 Leu Cys Leu Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln
 225 230 235 240
 Asp Ala Ala Phe Ala Phe Ala Ser Leu Ala Ile Val Phe Ser Ser Tyr
 245 250 255
 Ile Thr Leu Val Val Leu Phe Val Pro Lys Met
 260 265

<210> 9
 <211> 264
 <212> PRT
 <213> Human

<400> 9

Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala
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Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
 20 25 30
 Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
 35 40 45
 Leu Ser Tyr Ala Ser Ile Phe Leu Phe Gly Leu Asp Gly Ser Phe Val
 50 55 60
 Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val Arg Thr Trp Ile Leu
 65 70 75 80
 Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met Phe Ala Lys Thr Trp
 85 90 95
 Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Lys Ile Ile
 100 105 110
 Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
 115 120 125
 Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr
 130 135 140
 Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
 145 150 155 160
 Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp
 165 170 175
 Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys
 180 185 190
 Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile Pro Ala Leu Asn Asp
 195 200 205
 Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val Gly Ile Met Cys Ile
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 Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp Gln Pro Asn Val Gln
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 Cys Leu Val Phe Val Pro Lys Leu
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 <213> Human

<400> 11

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Lys Pro Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala
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His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val
      20           25           30

Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro
      35           40           45

Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln
 50           55           60

Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu
65           70           75           80

Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln
      85           90           95

Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr
      100          105          110

Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly
      115          120          125

Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr
      130          135          140

Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp
      145          150          155          160

Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly
      165          170          175

Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu
      180          185          190

Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr
      195          200          205

Val Thr Glu Asn Val Val Asn Ser
      210          215

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<210> 12
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 <212> PRT
 <213> Human

<400> 12

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Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr
 1           5           10           15

Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg
      20           25           30

Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys
      35           40           45

Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln
      50           55           60

Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly
65           70           75           80

Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly
      85           90           95

Ser Arg Val His Leu Leu Tyr Lys
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<210> 13
 <211> 104
 <212> PRT
 <213> Human

<400> 13

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Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu Ala Gln Asp Thr
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Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu Glu Lys Ser Arg
      20           25           30

Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile Ile Ala Glu Lys
      35           40           45

Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln Ser Arg Gln Gln
      50           55           60

Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Glu Pro Ser Gly Gly
65           70           75           80

Leu Pro Arg Gly Pro Pro Glu Pro Pro Asp Arg Leu Ser Cys Asp Gly
      85           90           95

Ser Arg Val His Leu Leu Tyr Lys
      100

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<210> 14
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 <212> PRT
 <213> Human

<400> 14

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Ile Thr Leu Arg Thr Asn Pro Asp Ala Ala Thr Gln Asn Arg Arg Phe
 1           5           10           15

Gln Phe Thr Gln Asn Gln Lys Lys Glu Asp Ser Lys Thr Ser Thr Ser
      20           25           30

Val Thr Ser Val Asn Gln Ala Ser Thr Ser Arg Leu Glu Gly Leu Gln
      35           40           45

Ser Glu Asn His Arg Leu Arg Met Lys Ile Thr Glu Leu Asp Lys Asp
 50           55           60

Leu Glu Glu Val Thr Met Gln Leu Gln Asp Thr Pro Glu Lys Thr Thr
 65           70           75           80

Tyr Ile Lys Gln Asn His Tyr Gln Glu Leu Asn Asp Ile Leu Asn Leu
      85           90           95

Gly Asn Phe Thr Glu Ser Thr Asp Gly Gly Lys Ala Ile Leu Lys Asn
      100          105          110

His Leu Asp Gln Asn Pro Gln Leu Gln Trp Asn Thr Thr Glu Pro Ser
      115          120          125

Arg Thr Cys Lys Asp Pro Ile Glu Asp Ile Asn Ser Pro Glu His Ile
      130          135          140

Gln Arg Arg Leu Ser Leu Gln Leu Pro Ile Leu His His Ala Tyr Leu
      145          150          155          160

Pro Ser Ile Gly Gly Val Asp Ala Ser Cys Val Ser Pro Cys Val Ser
      165          170          175

Pro Thr Ala Ser Pro Arg His Arg His Val Pro Pro Ser Phe Arg Val
      180          185          190

Met Val Ser Gly Leu
      195

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 <212> PRT
 <213> Human

<400> 15

His Pro Glu Gln Asn Val Gln Lys Arg Lys Arg Ser Phe Lys Ala Val
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 Val Thr Ala Ala Thr Met Gln Ser Lys Leu Ile Gln Lys Gly Asn Asp
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 Arg Pro Asn Gly Glu Val Lys Ser Glu Leu Cys Glu Ser Leu Glu Thr
 35 40 45
 Asn Ser Lys Ser Ser Val Glu Phe Pro Met Val Lys Ser Gly Ser Thr
 50 55 60
 Ser
 65

<210> 16
 <211> 374
 <212> PRT
 <213> Human

<400> 16

Met Ala Arg Ser Leu Thr Trp Gly Cys Cys Pro Trp Cys Leu Thr Glu
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 Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu Leu
 35 40 45
 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
 50 55 60
 Ile His Gly Val Gly Tyr Ser Glu Glu Asp Arg Arg Ala Phe Arg Leu
 65 70 75 80
 Leu Ile Tyr Gln Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala
 85 90 95
 Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His
 100 105 110
 Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu
 115 120 125
 Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile
 130 135 140

Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
 145 150 155 160
 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile
 165 170 175
 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
 180 185 190
 Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp
 195 200 205
 Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu
 210 215 220
 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
 225 230 235 240
 Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala
 245 250 255
 Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
 260 265 270
 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr
 275 280 285
 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp
 290 295 300
 Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr
 305 310 315 320
 Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala
 325 330 335
 Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val
 340 345 350
 Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
 355 360 365
 Asp Glu Ile Asn Leu Leu
 370

<210> 17
 <211> 374
 <212> PRT
 <213> Human

<400> 17

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Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
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Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
 20          25          30

Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu
 35          40          45

Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
 50          55          60

Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
 65          70          75          80

Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
          85          90          95

Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
          100          105          110

Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
          115          120          125

Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
          130          135          140

Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
          145          150          155          160

Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
          165          170          175

Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
          180          185          190

Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
          195          200          205

Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
          210          215          220

Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
          225          230          235          240

Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
          245          250          255

Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
          260          265          270

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Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
 275 280 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
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Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
 305 310 315 320

Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser
 325 330 335

Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
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Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
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Asp Glu Ile Asn Leu Leu
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 <212> DNA
 <213> Human

<400> 18

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His	Pro	Pro 35	Trp	Glu	Gly	Gly	Ile 40	Arg	Tyr	Arg	Gly	Leu 45	Thr	Arg	Asp
Gln	Val 50	Lys	Ala	Ile	Asn	Phe 55	Leu	Pro	Val	Asp	Tyr 60	Glu	Ile	Glu	Tyr
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Leu	Thr	Gly 115	Gly	Asp	Leu	Pro	Ala 120	Leu	Asp	Gly	Ala	Arg 125	Val	Glu	Phe
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Ser 145	Gln	Gly	Gln	Trp	Ser	Thr	Pro	Lys	Pro	His 155	Cys	Gln	Val	Asn	Arg 160
Thr	Pro	His	Ser 165	Glu	Arg	Arg	Ala	Val	Tyr 170	Ile	Gly	Ala	Leu	Phe	Pro
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Glu 210	Leu	Lys	Leu	Ile	His	His 215	Asp	Ser	Lys	Cys	Asp 220	Pro	Gly	Gln	Ala
Thr 225	Lys	Tyr	Leu	Tyr	Glu 230	Leu	Leu	Tyr	Asn	Asp 235	Pro	Ile	Lys	Ile	Ile 240
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 Gln Phe Pro Phe Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly
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 Thr Val Phe Thr Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu
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 Glu Pro Trp Lys Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp
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 740 745 750
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 755 760 765
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 785 790 795 800
 His Arg Ala Val Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu
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 Ile Thr Ala Pro Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala
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 Val Val Leu Phe Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu
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Pro	His 35	Leu	Pro	Arg	Pro	His	Pro 40	Arg	Val	Pro	Pro	His 45	Pro	Ser	Ser
Glu 50	Arg	Arg	Ala	Val	Tyr	Ile 55	Gly	Ala	Leu	Phe	Pro 60	Met	Ser	Gly	Gly
Trp 65	Pro	Gly	Gly	Gln 70	Ala	Cys	Gln	Pro	Ala 75	Val	Glu	Met	Ala	Leu	Glu 80
Asp	Val	Asn	Ser 85	Arg	Arg	Asp	Ile	Leu 90	Pro	Asp	Tyr	Glu	Leu 95	Lys	Leu
Ile	His	His 100	Asp	Ser	Lys	Cys	Asp 105	Pro	Gly	Gln	Ala	Thr 110	Lys	Tyr	Leu
Tyr	Glu 115	Leu	Leu	Tyr	Asn	Asp	Pro 120	Ile	Lys	Ile	Ile 125	Leu	Met	Pro	Gly
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Ser 225	Phe	Phe	Ser	Asp	Pro 230	Ala	Val	Pro	Val	Lys 235	Asn	Leu	Lys	Arg	Gln 240	
Asp	Ala	Arg	Ile	Ile 245	Val	Gly	Leu	Phe	Tyr 250	Glu	Thr	Glu	Ala	Arg 255	Lys	
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Ile	Gly 435	Tyr	Tyr	Asp	Ser	Thr	Lys 440	Asp	Asp	Leu	Ser	Trp 445	Ser	Lys	Thr	
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 Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val
 675 680 685
 Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro
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 Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu
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 Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu

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Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala
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Met Leu Phe Ala Leu Asp Arg Ile Asn Arg Asp Pro His Leu Leu Pro
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Gly Ala Asp Gly Ser Arg His Ile Cys Pro Asp Gly Ser Tyr Ala Thr
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His Gly Asp Ala Pro Thr Ala Ile Thr Gly Val Ile Gly Gly Ser Tyr
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Val Gly Arg Ala Met Ser Arg Ala Ala Phe Glu Gly Val Val Arg Ala		
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Ser Tyr Pro Ile Ser Asp Phe Ala Ser Tyr Phe Gln Ser Leu Asp Pro		
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Ala Val Pro Phe Glu Gln Glu Ser Lys Ile Met Phe Val Val Asn Ala		
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Val Tyr Ala Met Ala His Ala Leu His Asn Met His Arg Ala Leu Cys		
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Pro Asn Thr Thr Arg Leu Cys Asp Ala Met Arg Pro Val Asn Gly Arg		
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Arg Leu Tyr Lys Asp Phe Val Leu Asn Val Lys Phe Asp Ala Pro Phe		
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Arg Pro Ala Asp Thr His Asn Glu Val Arg Phe Asp Arg Phe Gly Asp		
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Gln	Pro	Gly	Glu	Val	Cys	Cys	Trp	Leu	Cys	Ile	Pro	Cys	Gln	Pro	Tyr
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Glu	Tyr	Arg	Leu	Asp	Glu	Phe	Thr	Cys	Ala	Asp	Cys	Gly	Leu	Gly	Tyr
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Trp	Pro	Asn	Ala	Ser	Leu	Thr	Gly	Cys	Phe	Glu	Leu	Pro	Gln	Glu	Tyr
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Ser Asp Tyr Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu
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<223> Chimeric Gqi5

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<213> Artificial Sequence

<220>
<223> Chimeric Gqi5

<400> 29

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Asp	Lys	Ile	Ile	Tyr	Ser	His	Phe	Thr	Cys	Ala	Thr	Asp	Thr	Glu	Asn
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345

350

Leu Lys Asp Cys Gly Leu Phe
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<223> Chimeric hCAR/hmGluR2

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<213> Artificial Sequence

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<223> Chimeric hCAR/hmGluR2

<400> 31

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      50             55             60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
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Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
          85             90             95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
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Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
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Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
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Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
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Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
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 Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
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 Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
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 385 390 395 400
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<223> Chimeric phCaR/hmGluR2*Gqi5

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<210> 33
 <211> 1276
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Chimeric phCaR/hmGluR2*Gqi5

 <400> 33

Met	Ala	Phe	Tyr	Ser	Cys	Cys	Trp	Val	Leu	Leu	Ala	Leu	Thr	Trp	His	1	5	10	15
Thr	Ser	Ala	Tyr	Gly	Pro	Asp	Gln	Arg	Ala	Gln	Lys	Lys	Gly	Asp	Ile	20	25	30	
Ile	Leu	Gly	Gly	Leu	Phe	Pro	Ile	His	Phe	Gly	Val	Ala	Ala	Lys	Asp	35	40	45	
Gln	Asp	Leu	Lys	Ser	Arg	Pro	Glu	Ser	Val	Glu	Cys	Ile	Arg	Tyr	Asn	50	55	60	
Phe	Arg	Gly	Phe	Arg	Trp	Leu	Gln	Ala	Met	Ile	Phe	Ala	Ile	Glu	Glu	65	70	75	80
Ile	Asn	Ser	Ser	Pro	Ala	Leu	Leu	Pro	Asn	Leu	Thr	Leu	Gly	Tyr	Arg	85	90	95	
Ile	Phe	Asp	Thr	Cys	Asn	Thr	Val	Ser	Lys	Ala	Leu	Glu	Ala	Thr	Leu	100	105	110	
Ser	Phe	Val	Ala	Gln	Asn	Lys	Ile	Asp	Ser	Leu	Asn	Leu	Asp	Glu	Phe	115	120	125	
Cys	Asn	Cys	Ser	Glu	His	Ile	Pro	Ser	Thr	Ile	Ala	Val	Val	Gly	Ala	130	135	140	
Thr	Gly	Ser	Gly	Val	Ser	Thr	Ala	Val	Ala	Asn	Leu	Leu	Gly	Leu	Phe	145	150	155	160
Tyr	Ile	Pro	Gln	Val	Ser	Tyr	Ala	Ser	Ser	Ser	Arg	Leu	Leu	Ser	Asn	165	170	175	
Lys	Asn	Gln	Phe	Lys	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	Glu	His	180	185	190	
Gln	Ala	Thr	Ala	Met	Ala	Asp	Ile	Ile	Glu	Tyr	Phe	Arg	Trp	Asn	Trp	195	200	205	
Val	Gly	Thr	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	Pro	Gly	Ile	Glu	210	215	220	
Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	Asp	Phe	Ser	225	230	235	240
Glu	Leu	Ile	Ser	Gln	Tyr	Ser	Asp	Glu	Glu	Glu	Ile	Gln	His	Val	Val	245	250	255	

Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
 260 265 270
 Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
 275 280 285
 Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
 290 295 300
 Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
 305 310 315 320
 Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
 325 330 335
 Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
 340 345 350
 Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
 355 360 365
 Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
 370 375 380
 Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
 385 390 395 400
 Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
 405 410 415
 Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
 420 425 430
 Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
 435 440 445
 Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
 450 455 460
 Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
 465 470 475 480
 Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
 485 490 495
 Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
 500 505 510
 Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
 515 520 525
 Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
 530 535 540
 Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr

545		550		555		560
Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu						
		565		570		575
Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn						
		580		585		590
Glu Asn His Thr Ser Cys Phe Glu Leu Pro Gln Glu Tyr Ile Arg Trp						
		595		600		605
Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys Leu Gly Ala						
		610		615		620
Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His Asn Ala Thr						
		625		630		635
Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile Leu Leu Gly						
		645		650		655
Gly Val Phe Leu Cys Tyr Cys Met Thr Phe Ile Phe Ile Ala Lys Pro						
		660		665		670
Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly Thr Ala Phe						
		675		680		685
Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg Ile Ala Arg						
		690		695		700
Ile Phe Gly Gly Ala Arg Glu Gly Ala Gln Arg Pro Arg Phe Ile Ser						
		705		710		715
Pro Ala Ser Gln Val Ala Ile Cys Leu Ala Leu Ile Ser Gly Gln Leu						
		725		730		735
Leu Ile Val Val Ala Trp Leu Val Val Glu Ala Pro Gly Thr Gly Lys						
		740		745		750
Glu Thr Ala Pro Glu Arg Arg Glu Val Val Thr Leu Arg Cys Asn His						
		755		760		765
Arg Asp Ala Ser Met Leu Gly Ser Leu Ala Tyr Asn Val Leu Leu Ile						
		770		775		780
Ala Leu Cys Thr Leu Tyr Ala Phe Asn Thr Arg Lys Cys Pro Glu Asn						
		785		790		795
Phe Asn Glu Ala Lys Phe Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile						
		805		810		815
Ile Trp Leu Ala Leu Leu Pro Ile Phe Tyr Val Thr Ser Ser Asp Tyr						
		820		825		830
Arg Val Gln Thr Thr Thr Met Cys Val Ser Val Ser Leu Ser Gly Ser						
		835		840		845

Val Val Leu Gly Cys Leu Phe Ala Pro Lys Leu His Ile Ile Leu Phe
 850 855 860
 Gln Pro Gln Lys Asn Val Val Ser His Arg Ala Pro Thr Ser Arg Phe
 865 870 875 880
 Gly Ser Ala Ala Ala Arg Ala Ser Ser Ser Leu Gly Gln Gly Ser Gly
 885 890 895
 Ser Gln Phe Val Pro Thr Val Cys Asn Gly Arg Glu Val Val Asp Ser
 900 905 910
 Thr Thr Ser Ser Leu Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu
 915 920 925
 Ser Glu Glu Ala Lys Glu Ala Arg Arg Ile Asn Asp Glu Ile Glu Arg
 930 935 940
 Gln Leu Arg Arg Asp Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu
 945 950 955 960
 Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met
 965 970 975
 Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe
 980 985 990
 Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile
 995 1000 1005
 Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys
 1010 1015 1020
 Ala His Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala
 1025 1030 1035 1040
 Phe Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro
 1045 1050 1055
 Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp
 1060 1065 1070
 Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala
 1075 1080 1085
 Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr
 1090 1095 1100
 Gly Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met
 1105 1110 1115 1120
 Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys
 1125 1130 1135
 Phe Glu Asn Val Thr Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr
 1140 1145 1150


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Asp Gln Val Leu Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser
    1155                      1160                      1165

Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser
    1170                      1175                      1180

Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile
    1185                      1190                      1195                      1200

Met Tyr Ser His Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln
    1205                      1210                      1215

Arg Asp Ala Gln Ala Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp
    1220                      1225                      1230

Leu Asn Pro Asp Ser Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala
    1235                      1240                      1245

Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp Thr
    1250                      1255                      1260

Ile Leu Gln Leu Asn Leu Lys Asp Cys Gly Leu Phe
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<210> 34
<211> 3105
<212> DNA
<213> Artificial Sequence

<220>
<223> Chimeric hmGluR2/hCaR

<400> 34

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ccagccaaga aggtgctgac cctggaggga gacttggtgc tgggtgggct gttcccagtg      120
caccagaagg gcggcccagc agaggactgt ggtcctgtca atgagcaccg tggcatccag      180
cgcttgagg ccattgctttt tgcaactggac cgcatacaacc gtgaccgcga cctgctgcct      240
ggcgtgcgcc tgggtgcaca catcctcgac agttgctcca aggacacaca tgcgctggag      300
caggcactgg actttgtgcg tgccctcactc agccgtgggtg ctgatggctc acgccacatc      360
tgccccgacg gctcttatgc gacccatggt gatgctccca ctgccatcac tgggtgttatt      420
ggcggttcct acagtgatgt ctccatccag gtggccaacc tcttgaggct atttcagatc      480
ccacagatta gctacgcctc taccagtgcc aagctgagtg acaagtcccg ctatgactac      540
tttggccgca cagtgcctcc tgacttcttc caagccaagg ccatggctga gattctccgc      600
ttcttcaact ggacctatgt gtccactgtg gcgtctgagg gcgactatgg cgagacaggc      660
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gtgggcccgtg ccatgagccg cgcggccttt gaggggtgtg tgcgagccct gctgcagaag      780
cccagtgcgc gcgtggctgt cctgttcacc cgttctgagg atgcccgga gctgcttgct      840
gccagccagc gcctcaatgc cagcttcacc tgggtggcca gtgatggttg gggggccctg      900
gagagtgtgg tggcaggcag tgagggggct gctgagggtg ctatcaccat cgagctggcc      960
tcctaccca tcagtgactt tgccctctac ttccagagcc tggacccttg gaacaacagc     1020
cggaaccctt ggttccgtga attctgggag cagaggttcc gctgcagctt ccggcagcga     1080
gactgcgcag cccactctct ccgggctgtg ccctttgagc aggagtccaa gatcatgttt     1140

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cccaacacca cccggctctg tgacgcgatg cggccagtta acgggcgcgc cctctacaag 1260
gacttttgtg tcaacgtcaa gtttgatgcc ccctttcgcc cagctgacac ccacaatgag 1320
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gcaggcagtg ggcgctatcg ctaccagaag gtgggctact gggcagaagg cttgactctg 1440
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gatctgaccg tccaggaaac aggtctgcaa ggacctgtgg gtggagacca gcggccagag 3000
gtggaggacc ctgaagagtt gtccccagca cttgtagtgt ccagttcaca gagctttgtc 3060
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<210> 35

<211> 1035

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric hmGluR2/hCaR

<400> 35

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Met Gly Ser Leu Leu Ala Leu Pro Ala Leu Leu Leu Leu Trp Gly Ala
 1             5             10             15

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Val Ala Glu Gly Pro Ala Lys Lys Val Leu Thr Leu Glu Gly Asp Leu
      20             25             30

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Val Leu Gly Gly Leu Phe Pro Val His Gln Lys Gly Gly Pro Ala Glu
      35             40             45

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Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala

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50					55					60					
Met	Leu	Phe	Ala	Leu	Asp	Arg	Ile	Asn	Arg	Asp	Pro	His	Leu	Leu	Pro
65					70					75					80
Gly	Val	Arg	Leu	Gly	Ala	His	Ile	Leu	Asp	Ser	Cys	Ser	Lys	Asp	Thr
				85					90					95	
His	Ala	Leu	Glu	Gln	Ala	Leu	Asp	Phe	Val	Arg	Ala	Ser	Leu	Ser	Arg
			100					105					110		
Gly	Ala	Asp	Gly	Ser	Arg	His	Ile	Cys	Pro	Asp	Gly	Ser	Tyr	Ala	Thr
		115					120					125			
His	Gly	Asp	Ala	Pro	Thr	Ala	Ile	Thr	Gly	Val	Ile	Gly	Gly	Ser	Tyr
	130					135					140				
Ser	Asp	Val	Ser	Ile	Gln	Val	Ala	Asn	Leu	Leu	Arg	Leu	Phe	Gln	Ile
145					150					155					160
Pro	Gln	Ile	Ser	Tyr	Ala	Ser	Thr	Ser	Ala	Lys	Leu	Ser	Asp	Lys	Ser
				165					170					175	
Arg	Tyr	Asp	Tyr	Phe	Ala	Arg	Thr	Val	Pro	Pro	Asp	Phe	Phe	Gln	Ala
			180					185					190		
Lys	Ala	Met	Ala	Glu	Ile	Leu	Arg	Phe	Phe	Asn	Trp	Thr	Tyr	Val	Ser
	195						200					205			
Thr	Val	Ala	Ser	Glu	Gly	Asp	Tyr	Gly	Glu	Thr	Gly	Ile	Glu	Ala	Phe
	210					215					220				
Glu	Leu	Glu	Ala	Arg	Ala	Arg	Asn	Ile	Cys	Val	Ala	Thr	Ser	Glu	Lys
225					230					235				240	
Val	Gly	Arg	Ala	Met	Ser	Arg	Ala	Ala	Phe	Glu	Gly	Val	Val	Arg	Ala
				245					250					255	
Leu	Leu	Gln	Lys	Pro	Ser	Ala	Arg	Val	Ala	Val	Leu	Phe	Thr	Arg	Ser
			260					265					270		
Glu	Asp	Ala	Arg	Glu	Leu	Leu	Ala	Ala	Ser	Gln	Arg	Leu	Asn	Ala	Ser
	275						280					285			
Phe	Thr	Trp	Val	Ala	Ser	Asp	Gly	Trp	Gly	Ala	Leu	Glu	Ser	Val	Val
	290					295					300				
Ala	Gly	Ser	Glu	Gly	Ala	Ala	Glu	Gly	Ala	Ile	Thr	Ile	Glu	Leu	Ala
305				310						315				320	
Ser	Tyr	Pro	Ile	Ser	Asp	Phe	Ala	Ser	Tyr	Phe	Gln	Ser	Leu	Asp	Pro
				325					330					335	
Trp	Asn	Asn	Ser	Arg	Asn	Pro	Trp	Phe	Arg	Glu	Phe	Trp	Glu	Gln	Arg
			340					345					350		

Phe Arg Cys Ser Phe Arg Gln Arg Asp Cys Ala Ala His Ser Leu Arg
 355 360 365
 Ala Val Pro Phe Glu Gln Glu Ser Lys Ile Met Phe Val Val Asn Ala
 370 375 380
 Val Tyr Ala Met Ala His Ala Leu His Asn Met His Arg Ala Leu Cys
 385 390 395 400
 Pro Asn Thr Thr Arg Leu Cys Asp Ala Met Arg Pro Val Asn Gly Arg
 405 410 415
 Arg Leu Tyr Lys Asp Phe Val Leu Asn Val Lys Phe Asp Ala Pro Phe
 420 425 430
 Arg Pro Ala Asp Thr His Asn Glu Val Arg Phe Asp Arg Phe Gly Asp
 435 440 445
 Gly Ile Gly Arg Tyr Asn Ile Phe Thr Tyr Leu Arg Ala Gly Ser Gly
 450 455 460
 Arg Tyr Arg Tyr Gln Lys Val Gly Tyr Trp Ala Glu Gly Leu Thr Leu
 465 470 475 480
 Asp Thr Ser Leu Ile Pro Trp Ala Ser Pro Ser Ala Gly Pro Leu Pro
 485 490 495
 Ala Ser Arg Cys Ser Glu Pro Cys Leu Gln Asn Glu Val Lys Ser Val
 500 505 510
 Gln Pro Gly Glu Val Cys Cys Trp Leu Cys Ile Pro Cys Gln Pro Tyr
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 Glu Tyr Arg Leu Asp Glu Phe Thr Cys Ala Asp Cys Gly Leu Gly Tyr
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 Trp Pro Asn Ala Ser Leu Thr Gly Cys Phe Glu Leu Pro Gln Glu Tyr
 545 550 555 560
 Ile Arg Trp Gly Asp Ala Trp Ala Val Gly Pro Val Thr Ile Ala Cys
 565 570 575
 Leu Gly Ala Leu Ala Thr Leu Phe Val Leu Gly Val Phe Val Arg His
 580 585 590
 Asn Ala Thr Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile
 595 600 605
 Leu Leu Gly Gly Val Phe Leu Cys Tyr Cys Met Thr Phe Ile Phe Ile
 610 615 620
 Ala Lys Pro Ser Thr Ala Val Cys Thr Leu Arg Arg Leu Gly Leu Gly
 625 630 635 640
 Thr Ala Phe Ser Val Cys Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg

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Ile	Ala	Arg	Ile	Phe	Gly	Gly	Ala	Arg	Glu	Gly	Ala	Gln	Arg	Pro	Arg						
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Phe	Ile	Ser	Pro	Ala	Ser	Gln	Val	Ala	Ile	Cys	Leu	Ala	Leu	Ile	Ser						
		675					680					685									
Gly	Gln	Leu	Leu	Ile	Val	Val	Ala	Trp	Leu	Val	Val	Glu	Ala	Pro	Gly						
	690					695					700										
Thr	Gly	Lys	Glu	Thr	Ala	Pro	Glu	Arg	Arg	Glu	Val	Val	Thr	Leu	Arg						
705					710					715					720						
Cys	Asn	His	Arg	Asp	Ala	Ser	Met	Leu	Gly	Ser	Leu	Ala	Tyr	Asn	Val						
				725					730					735							
Leu	Leu	Ile	Ala	Leu	Cys	Thr	Leu	Tyr	Ala	Phe	Lys	Thr	Arg	Lys	Cys						
			740					745					750								
Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys	Phe	Ile	Gly	Phe	Thr	Met	Tyr	Thr						
		755					760					765									
Thr	Cys	Ile	Ile	Trp	Leu	Ala	Phe	Leu	Pro	Ile	Phe	Tyr	Val	Thr	Ser						
	770					775					780										
Ser	Asp	Tyr	Arg	Val	Gln	Thr	Thr	Thr	Met	Cys	Val	Ser	Val	Ser	Leu						
785					790					795					800						
Ser	Gly	Ser	Val	Val	Leu	Gly	Cys	Leu	Phe	Ala	Pro	Lys	Leu	His	Ile						
			805						810					815							
Ile	Leu	Phe	Gln	Pro	Gln	Lys	Asn	Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser						
			820					825					830								
Thr	Ala	Ala	His	Ala	Phe	Lys	Val	Ala	Ala	Arg	Ala	Thr	Leu	Arg	Arg						
	835						840					845									
Ser	Asn	Val	Ser	Arg	Lys	Arg	Ser	Ser	Ser	Leu	Gly	Gly	Ser	Thr	Gly						
	850					855					860										
Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser	Ser	Lys	Ser	Asn	Ser	Glu	Asp	Pro						
865					870					875				880							
Phe	Pro	Gln	Pro	Glu	Arg	Gln	Lys	Gln	Gln	Gln	Pro	Leu	Ala	Leu	Thr						
			885					890						895							
Gln	Gln	Glu	Gln	Gln	Gln	Gln	Pro	Leu	Thr	Leu	Pro	Gln	Gln	Gln	Arg						
		900						905					910								
Ser	Gln	Gln	Gln	Pro	Arg	Cys	Lys	Gln	Lys	Val	Ile	Phe	Gly	Ser	Gly						
	915						920					925									
Thr	Val	Thr	Phe	Ser	Leu	Ser	Phe	Asp	Glu	Pro	Gln	Lys	Asn	Ala	Met						
	930					935					940										

Ala His Gly Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser
 945 950 955 960

Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly
 965 970 975

Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro
 980 985 990

Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser
 995 1000 1005

Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly
 1010 1015 1020

Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser
 1025 1030 1035

<210> 36
 <211> 4185
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric pmGluR2//CaR*G(qi5

<400> 36

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caccagaagg	gcgggccagc	agaggactgt	ggtcctgtca	atgagcaccg	tggcatccag	180
cgcttgagg	ccatgctttt	tgcactggac	cgcacacacc	gtgacccgca	cctgctgcct	240
ggcgtgcgcc	tgggtgcaca	catcctcgac	agttgctcca	aggacacaca	tgcgctggag	300
caggcactgg	actttgtgcg	tgcctcactc	agcctggttg	ctgatggctc	acgccacatc	360
tgccccgacg	gctcttatgc	gacccatggt	gatgctccca	ctgccatcac	tgggtgtatt	420
ggcggttcct	acagtgatgt	ctccatccag	gtggccaacc	tcttgaggct	atttcagatc	480
ccacagatta	gctacgcctc	taccagtgcc	aagctgagtg	acaagtcccg	ctatgactac	540
tttggccgca	cagtgcctcc	tgacttcttc	caagccaagg	ccatggctga	gattctccgc	600
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<211> 1394

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric pmGluR2//CaR*G(qi5

<400> 37

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Val	Leu	Gly	Gly	Leu	Phe	Pro	Val	His	Gln	Lys	Gly	Gly	Pro	Ala	Glu	35	40	45	
Asp	Cys	Gly	Pro	Val	Asn	Glu	His	Arg	Gly	Ile	Gln	Arg	Leu	Glu	Ala	50	55	60	
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Gly	Val	Arg	Leu	Gly	Ala	His	Ile	Leu	Asp	Ser	Cys	Ser	Lys	Asp	Thr	85	90	95	
His	Ala	Leu	Glu	Gln	Ala	Leu	Asp	Phe	Val	Arg	Ala	Ser	Leu	Ser	Arg	100	105	110	
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Ser	Asp	Val	Ser	Ile	Gln	Val	Ala	Asn	Leu	Leu	Arg	Leu	Phe	Gln	Ile	145	150	155	160
Pro	Gln	Ile	Ser	Tyr	Ala	Ser	Thr	Ser	Ala	Lys	Leu	Ser	Asp	Lys	Ser	165	170	175	
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Glu	Asp	Ala	Arg	Glu	Leu	Leu	Ala	Ala	Ser	Gln	Arg	Leu	Asn	Ala	Ser	275	280	285	

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 690 695 700
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<211> 1059
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 <213> Artificial Sequence

<220>
 <223> Chimeric hmGluR8/hCaR

<400> 39

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Ser	Gln	Glu	Tyr	Ala	His	Ser	Ile	Arg	Val	Asp	Gly	Asp	Ile	Ile	Leu	35	40	45	
Gly	Gly	Leu	Phe	Pro	Val	His	Ala	Lys	Gly	Glu	Arg	Gly	Val	Pro	Cys	50	55	60	
Gly	Glu	Leu	Lys	Lys	Glu	Lys	Gly	Ile	His	Arg	Leu	Glu	Ala	Met	Leu	65	70	75	80
Tyr	Ala	Ile	Asp	Gln	Ile	Asn	Lys	Asp	Pro	Asp	Leu	Leu	Ser	Asn	Ile	85	90	95	
Thr	Leu	Gly	Val	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala	100	105	110	
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp	Ala	115	120	125	
Ser	Asp	Val	Lys	Cys	Ala	Asn	Gly	Asp	Pro	Pro	Ile	Phe	Thr	Lys	Pro	130	135	140	
Asp	Lys	Ile	Ser	Gly	Val	Ile	Gly	Ala	Ala	Ala	Ser	Ser	Val	Ser	Ile	145	150	155	160
Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr	165	170	175	
Ala	Ser	Thr	Ala	Pro	Glu	Leu	Ser	Asp	Asn	Thr	Arg	Tyr	Asp	Phe	Phe	180	185	190	
Ser	Arg	Val	Val	Pro	Pro	Asp	Ser	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp	195	200	205	
Ile	Val	Thr	Ala	Leu	Gly	Trp	Asn	Tyr	Val	Ser	Thr	Leu	Ala	Ser	Glu	210	215	220	
Gly	Asn	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Thr	Gln	Ile	Ser	Arg	225	230	235	240
Glu	Ile	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Gln	Lys	Ile	Pro	Arg	Glu	245	250	255	

1059
 PRT
 Artificial Sequence
 Chimeric hmGluR8/hCaR
 39

Pro Arg Pro Gly Glu Phe Glu Lys Ile Ile Lys Arg Leu Leu Glu Thr
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 Pro Asn Ala Arg Ala Val Ile Met Phe Ala Asn Glu Asp Asp Ile Arg
 275 280 285
 Arg Ile Leu Glu Ala Ala Lys Lys Leu Asn Gln Ser Gly His Phe Leu
 290 295 300
 Trp Ile Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Tyr Gln
 305 310 315 320
 Gln Glu Glu Ile Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Ala
 325 330 335
 Ser Ile Asp Gly Phe Asp Arg Tyr Phe Arg Ser Arg Thr Leu Ala Asn
 340 345 350
 Asn Arg Arg Asn Val Trp Phe Ala Glu Phe Trp Glu Glu Asn Phe Gly
 355 360 365
 Cys Lys Leu Gly Ser His Gly Lys Arg Asn Ser His Ile Lys Lys Cys
 370 375 380
 Thr Gly Leu Glu Arg Ile Ala Arg Asp Ser Ser Tyr Glu Gln Glu Gly
 385 390 395 400
 Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ser Met Ala Tyr Ala Leu
 405 410 415
 His Asn Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro
 420 425 430
 Arg Met Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala
 435 440 445
 Val Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Thr Phe Asn Glu Asn
 450 455 460
 Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Ile Thr Asn
 465 470 475 480
 Lys Ser Thr Glu Tyr Lys Val Ile Gly His Trp Thr Asn Gln Leu His
 485 490 495
 Leu Lys Val Glu Asp Met Gln Trp Ala His Arg Glu His Thr His Pro
 500 505 510
 Ala Ser Val Cys Ser Leu Pro Cys Lys Pro Gly Glu Arg Lys Lys Thr
 515 520 525
 Val Lys Gly Val Pro Cys Cys Trp His Cys Glu Arg Cys Glu Gly Tyr
 530 535 540
 Asn Tyr Gln Val Asp Glu Leu Ser Cys Glu Leu Cys Pro Leu Asp Gln
 545 550 555 560

Arg	Pro	Asn	Met	Asn	Arg	Thr	Gly	Cys	Gln	Leu	Ile	Pro	Ile	Ile	Lys	565	570	575
Leu	Glu	Trp	His	Ser	Pro	Trp	Ala	Val	Val	Pro	Val	Phe	Val	Ala	Ile	580	585	590
Leu	Gly	Ile	Ile	Ala	Thr	Thr	Phe	Val	Ile	Val	Thr	Phe	Val	Arg	Tyr	595	600	605
Asn	Asp	Thr	Pro	Ile	Val	Arg	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	Val	610	615	620
Leu	Leu	Thr	Gly	Ile	Phe	Leu	Cys	Tyr	Ser	Ile	Thr	Phe	Leu	Met	Ile	625	630	635
Ala	Ala	Pro	Asp	Thr	Ile	Ile	Cys	Ser	Phe	Arg	Arg	Val	Phe	Leu	Gly	645	650	655
Leu	Gly	Met	Cys	Phe	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg	660	665	670
Ile	His	Arg	Ile	Phe	Glu	Gln	Gly	Lys	Lys	Ser	Val	Thr	Ala	Pro	Lys	675	680	685
Phe	Ile	Ser	Pro	Ala	Ser	Gln	Leu	Val	Ile	Thr	Phe	Ser	Leu	Ile	Ser	690	695	700
Val	Gln	Leu	Leu	Gly	Val	Phe	Val	Trp	Phe	Val	Val	Asp	Pro	Pro	His	705	710	715
Ile	Ile	Ile	Asp	Tyr	Gly	Glu	Gln	Arg	Thr	Leu	Asp	Pro	Glu	Lys	Ala	725	730	735
Arg	Gly	Val	Leu	Lys	Cys	Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	Ser	740	745	750
Leu	Gly	Tyr	Ser	Ile	Leu	Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala	Ile	755	760	765
Lys	Thr	Arg	Gly	Val	Pro	Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	Gly	770	775	780
Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Ile	Trp	Leu	Ala	Phe	Ile	Pro	Ile	785	790	795
Phe	Phe	Gly	Thr	Ala	Gln	Ser	Ala	Glu	Lys	Met	Tyr	Ile	Gln	Thr	Thr	805	810	815
Thr	Leu	Thr	Val	Ser	Met	Ser	Leu	Ser	Ala	Ser	Val	Ser	Leu	Gly	Met	820	825	830
Leu	Tyr	Met	Pro	Lys	Val	Tyr	Ile	Ile	Ile	Phe	His	Pro	Glu	Gln	Asn	835	840	845
Thr	Ile	Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val			

850 855 860
 Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser
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 Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser
 885 890 895
 Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys
 900 905 910
 Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Gln Pro
 915 920 925
 Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys
 930 935 940
 Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe
 945 950 955 960
 Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser Thr His Gln
 965 970 975
 Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln
 980 985 990
 Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val
 995 1000 1005
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 Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser
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<223> Chimeric mGluR8//CaR*G(qi5

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 cgggtggatg gggacattat tttggggggt ctcttccttg tccacgcaaa gggagagaga 180

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cgcacctctg	acacgtgctc	tagggacacc	tatgcttttg	agcagtctct	aacattcgtg	360
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<400> 41
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Leu	Thr	Ala	Lys 20	Phe	Tyr	Trp	Ile	Leu 25	Thr	Met	Met	Gln	Arg 30	Thr	His
Ser	Gln	Glu	Tyr 35	Ala	His	Ser	Ile	Arg 40	Val	Asp	Gly	Asp 45	Ile	Ile	Leu
Gly	Gly 50	Leu	Phe	Pro	Val	His 55	Ala	Lys	Gly	Glu	Arg 60	Gly	Val	Pro	Cys
Gly 65	Glu	Leu	Lys	Lys 70	Glu	Lys	Gly	Ile	His 75	Arg	Leu	Glu	Ala	Met	Leu 80
Tyr	Ala	Ile	Asp 85	Gln	Ile	Asn	Lys	Asp 90	Pro	Asp	Leu	Leu	Ser	Asn 95	Ile
Thr	Leu	Gly 100	Val	Arg	Ile	Leu	Asp 105	Thr	Cys	Ser	Arg	Asp 110	Thr	Tyr	Ala
Leu	Glu	Gln 115	Ser	Leu	Thr	Phe	Val 120	Gln	Ala	Leu	Ile	Glu 125	Lys	Asp	Ala
Ser	Asp 130	Val	Lys	Cys	Ala	Asn 135	Gly	Asp	Pro	Pro	Ile	Phe 140	Thr	Lys	Pro
Asp 145	Lys	Ile	Ser	Gly 150	Val	Ile	Gly	Ala	Ala 155	Ala	Ser	Ser	Val	Ser	Ile 160
Met	Val	Ala	Asn 165	Ile	Leu	Arg	Leu	Phe 170	Lys	Ile	Pro	Gln	Ile	Ser 175	Tyr
Ala	Ser	Thr 180	Ala	Pro	Glu	Leu	Ser 185	Asp	Asn	Thr	Arg	Tyr 190	Asp	Phe	Phe

Ser Arg Val Val Pro Pro Asp Ser Tyr Gln Ala Gln Ala Met Val Asp
 195 200 205
 Ile Val Thr Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu
 210 215 220
 Gly Asn Tyr Gly Glu Ser Gly Val Glu Ala Phe Thr Gln Ile Ser Arg
 225 230 235 240
 Glu Ile Gly Gly Val Cys Ile Ala Gln Ser Gln Lys Ile Pro Arg Glu
 245 250 255
 Pro Arg Pro Gly Glu Phe Glu Lys Ile Ile Lys Arg Leu Leu Glu Thr
 260 265 270
 Pro Asn Ala Arg Ala Val Ile Met Phe Ala Asn Glu Asp Asp Ile Arg
 275 280 285
 Arg Ile Leu Glu Ala Ala Lys Lys Leu Asn Gln Ser Gly His Phe Leu
 290 295 300
 Trp Ile Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Tyr Gln
 305 310 315 320
 Gln Glu Glu Ile Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Ala
 325 330 335
 Ser Ile Asp Gly Phe Asp Arg Tyr Phe Arg Ser Arg Thr Leu Ala Asn
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 Asn Arg Arg Asn Val Trp Phe Ala Glu Phe Trp Glu Glu Asn Phe Gly
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 Cys Lys Leu Gly Ser His Gly Lys Arg Asn Ser His Ile Lys Lys Cys
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 Thr Gly Leu Glu Arg Ile Ala Arg Asp Ser Ser Tyr Glu Gln Glu Gly
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 Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ser Met Ala Tyr Ala Leu
 405 410 415
 His Asn Met His Lys Asp Leu Cys Pro Gly Tyr Ile Gly Leu Cys Pro
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 Arg Met Ser Thr Ile Asp Gly Lys Glu Leu Leu Gly Tyr Ile Arg Ala
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 Val Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Thr Phe Asn Glu Asn
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 Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Ile Thr Asn
 465 470 475 480

Lys Ser Thr Glu Tyr Lys Val Ile Gly His Trp Thr Asn Gln Leu His
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 Leu Lys Val Glu Asp Met Gln Trp Ala His Arg Glu His Thr His Pro
 500 505 510
 Ala Ser Val Cys Ser Leu Pro Cys Lys Pro Gly Glu Arg Lys Lys Thr
 515 520 525
 Val Lys Gly Val Pro Cys Cys Trp His Cys Glu Arg Cys Glu Gly Tyr
 530 535 540
 Asn Tyr Gln Val Asp Glu Leu Ser Cys Glu Leu Cys Pro Leu Asp Gln
 545 550 555 560
 Arg Pro Asn Met Asn Arg Thr Gly Cys Gln Leu Ile Pro Ile Ile Lys
 565 570 575
 Leu Glu Trp His Ser Pro Trp Ala Val Val Pro Val Phe Val Ala Ile
 580 585 590
 Leu Gly Ile Ile Ala Thr Thr Phe Val Ile Val Thr Phe Val Arg Tyr
 595 600 605
 Asn Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val
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 Ala Ala Pro Asp Thr Ile Ile Cys Ser Phe Arg Arg Val Phe Leu Gly
 645 650 655
 Leu Gly Met Cys Phe Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg
 660 665 670
 Ile His Arg Ile Phe Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Lys
 675 680 685
 Phe Ile Ser Pro Ala Ser Gln Leu Val Ile Thr Phe Ser Leu Ile Ser
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 Val Gln Leu Leu Gly Val Phe Val Trp Phe Val Val Asp Pro Pro His
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 Ile Ile Ile Asp Tyr Gly Glu Gln Arg Thr Leu Asp Pro Glu Lys Ala
 725 730 735
 Arg Gly Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Ser
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 Lys Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly
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Phe Thr Met Tyr Thr Thr Cys Ile Ile Trp Leu Ala Phe Ile Pro Ile
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Phe Phe Gly Thr Ala Gln Ser Ala Glu Lys Met Tyr Ile Gln Thr Thr
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Thr Leu Thr Val Ser Met Ser Leu Ser Ala Ser Val Ser Leu Gly Met
820 825 830

Leu Tyr Met Pro Lys Val Tyr Ile Ile Ile Phe His Pro Glu Gln Asn
835 840 845

Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys Val
850 855 860

Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser
865 870 875 880

Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser
885 890 895

Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys
900 905 910

Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln Gln Pro
915 920 925

Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys
930 935 940

Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe
945 950 955 960

Asp Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser Thr His Gln
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Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln
980 985 990

Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val
995 1000 1005

Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu
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Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser
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Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val
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Val Asn Ser Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu Ser Glu
1060 1065 1070

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Ile His Gly Ser Gly Tyr Ser Asp 1125	Glu Asp Lys Arg Gly Phe Thr 1130 1135	
Leu Val Tyr Gln Asn Ile Phe Thr 1140	Ala Met Gln Ala Met 1145 1150	Ile Arg Ala
Met Asp Thr Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala His 1155 1160 1165		
Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe Glu 1170 1175 1180		
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Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Thr 1205 1210 1215		
Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr Leu 1220 1225 1230		
Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile 1235 1240 1245		
Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val Asp 1250 1255 1260		
Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu 1265 1270 1275 1280		
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Val Leu Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala 1300 1305 1310		
Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val 1315 1320 1325		
Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr 1330 1335 1340		
Ser His Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp 1345 1350 1355 1360		
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<212> PRT

<213> Artificial Sequence

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<223> Chimeric GABA-BR2*Gqo5

<400> 43

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Leu Pro Leu Ala Pro Gly Ala Trp Gly Trp Ala Arg Gly Ala Pro Arg
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Pro Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu
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 995 1000 1005
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<213> Artificial Sequence

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<223> Chimeric GABA-BR1a*Gqo5

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<223> Chimeric GABA-BRa1*Gqo5

<400> 45

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Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
 35             40             45

Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu

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Ile	Leu	Met	Pro	Gly	Cys	Ser	Ser	Val	Ser	Thr	Leu	Val	Ala	Glu	Ala
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Phe	Lys	Ile	Tyr	Asp	Pro	Ser	Ile	Asn	Cys	Thr	Val	Asp	Glu	Met	Thr
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 Pro Thr Pro Pro Glu Pro Ser Gly Gly Leu Pro Arg Gly Pro Pro Glu
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 Pro Pro Asp Arg Leu Ser Cys Asp Gly Ser Arg Val His Leu Leu Tyr

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Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg			
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Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr			
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Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg			
	1045	1050	1055
Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala			
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His Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe			
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Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly			
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Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser			
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Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr			
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Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly			
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Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val			
	1155	1160	1165
Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe			
	1170	1175	1180
Glu Asn Val Thr Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp			
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Gln Val Leu Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys			
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Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser			
	1220	1225	1230
Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met			
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Tyr Ser His Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg
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 Asn Pro Asp Ser Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr
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 35 40 45
 Asp Cys Gly Pro Val Asn Glu His Arg Gly Ile Gln Arg Leu Glu Ala
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 Gly Val Arg Leu Gly Ala His Ile Leu Asp Ser Cys Ser Lys Asp Thr
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 Pro Gln Ile Ser Tyr Ala Ser Thr Ser Ala Lys Leu Ser Asp Lys Ser
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 210 215 220
 Glu Leu Glu Ala Arg Ala Arg Asn Ile Cys Val Ala Thr Ser Glu Lys
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 Val Gly Arg Ala Met Ser Arg Ala Ala Phe Glu Gly Val Val Arg Ala
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 Leu Leu Gln Lys Pro Ser Ala Arg Val Ala Val Leu Phe Thr Arg Ser
 260 265 270
 Glu Asp Ala Arg Glu Leu Leu Ala Ala Ser Gln Arg Leu Asn Ala Ser
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 Phe Thr Trp Val Ala Ser Asp Gly Trp Gly Ala Leu Glu Ser Val Val
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Phe Arg Cys Ser Phe Arg Gln Arg Asp Cys Ala Ala His Ser Leu Arg						
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Pro Asn Thr Thr Arg Leu Cys Asp Ala Met Arg Pro Val Asn Gly Arg						
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Arg Pro Ala Asp Thr His Asn Glu Val Arg Phe Asp Arg Phe Gly Asp						
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Gly Ile Gly Arg Tyr Asn Ile Phe Thr Tyr Leu Arg Ala Gly Ser Gly						
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Glu Tyr Arg Leu Asp Glu Phe Thr Cys Ala Asp Cys Gly Leu Gly Tyr						
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Trp Pro Asn Ala Ser Leu Thr Gly Cys Phe Glu Leu Pro Gln Glu Tyr						
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Asn Ala Thr Pro Val Val Lys Ala Ser Gly Arg Glu Leu Cys Tyr Ile						
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225				230						235					240
Glu	Asp	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Val	Lys	Ile	Pro	Arg	Glu
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Pro	Lys	Ala	Gly	Glu	Phe	Asp	Lys	Ile	Ile	Arg	Arg	Leu	Leu	Glu	Thr
			260					265					270		
Ser	Asn	Ala	Arg	Ala	Val	Ile	Ile	Phe	Ala	Asn	Glu	Asp	Asp	Ile	Arg
		275					280					285			
Arg	Val	Leu	Glu	Ala	Ala	Arg	Arg	Ala	Asn	Gln	Thr	Gly	His	Phe	Phe
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Trp	Met	Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Leu	His
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Leu	Glu	Glu	Val	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Met
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Ser	Val	Arg	Gly	Phe	Asp	Arg	Tyr	Phe	Ser	Ser	Arg	Thr	Leu	Asp	Asn
			340					345					350		
Asn	Arg	Arg	Asn	Ile	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Asp	Asn	Phe	His
		355					360					365			
Cys	Lys	Leu	Ser	Arg	His	Ala	Leu	Lys	Lys	Gly	Ser	His	Val	Lys	Lys
	370					375					380				
Cys	Thr	Asn	Arg	Glu	Arg	Ile	Gly	Gln	Asp	Ser	Ala	Tyr	Glu	Gln	Glu
385				390						395					400
Gly	Lys	Val	Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ala	Met	Gly	His	Ala
				405					410					415	
Leu	His	Ala	Met	His	Arg	Asp	Leu	Cys	Pro	Gly	Arg	Val	Gly	Leu	Cys
			420					425					430		
Pro	Arg	Met	Asp</												

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Tyr Gln Tyr Gln Val Asp Arg Tyr Thr Cys Lys Thr Cys Pro Tyr Asp				
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Met Arg Pro Thr Glu Asn Arg Thr Gly Cys Arg Pro Ile Pro Ile Ile				
		565		570
Lys Leu Glu Trp Gly Ser Pro Trp Ala Val Leu Pro Leu Phe Leu Ala				
		580		585
Val Val Gly Ile Ala Ala Thr Leu Phe Val Val Ile Thr Phe Val Arg				
		595		600
Tyr Asn Asp Thr Pro Ile Val Lys Ala Ser Gly Arg Glu Leu Ser Tyr				
		610		615
Val Leu Leu Ala Gly Ile Phe Leu Cys Tyr Ala Thr Thr Phe Leu Met				
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Ile Ala Glu Pro Asp Leu Gly Thr Cys Ser Leu Arg Arg Ile Phe Leu				
		645		650
Gly Leu Gly Met Ser Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn				
		660		665
Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys Arg Ser Val Ser Ala Pro				
		675		680
Arg Phe Ile Ser Pro Ala Ser Gln Leu Ala Ile Thr Phe Ser Leu Ile				
		690		695
Ser Leu Gln Leu Leu Gly Ile Cys Val Trp Phe Val Val Asp Pro Ser				
705		710		715
His Ser Val Val Asp Phe Gln Asp Gln Arg Thr Leu Asp Pro Arg Phe				
		725		730
Arg Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Leu Leu				
		740		745
Gly Tyr Ser Met Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile Lys				
		755		760
Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly Phe				
		770		775
Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile Phe				
785		790		795
Phe Gly Thr Ser Gln Ser Ala Asp Lys Leu Tyr Ile Gln Thr Thr Thr				
		805		810
Leu Thr Val Ser Val Ser Leu Ser Ala Ser Val Ser Leu Gly Met Leu				
		820		825
Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His Pro Glu Gln Asn Val				
		835		840
Pro Lys Arg Lys Arg Ser Leu Lys Ala Val Val Thr Ala Ala Thr Met				
		850		855
Ser Asn Lys Phe Thr Gln Lys Gly Asn Phe Arg Pro Asn Gly Glu Ala				
865		870		875
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 35 40 45
 Gly Gly Leu Phe Pro Val His Gly Arg Gly Ser Glu Gly Lys Pro Cys
 50 55 60
 Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu Ala Met Leu
 65 70 75 80
 Phe Ala Leu Asp Arg Ile Asn Asn Asp Pro Asp Leu Leu Pro Asn Ile
 85 90 95
 Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr His Ala
 100 105 110
 Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu Lys Asp Gly
 115 120 125
 Thr Glu Val Arg Cys Gly Ser Gly Gly Pro Pro Ile Ile Thr Lys Pro
 130 135 140
 Glu Arg Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser Val Ser Ile
 145 150 155 160
 Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln Ile Ser Tyr
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 Ala Ser Thr Ala Pro Asp Leu Ser Asp Asn Ser Arg Tyr Asp Phe Phe
 180 185 190
 Ser Arg Val Val Pro Ser Asp Thr Tyr Gln Ala Gln Ala Met Val Asp
 195 200 205
 Ile Val Arg Ala Leu Lys Trp Asn Tyr Val Ser Thr Val Ala Ser Glu
 210 215 220
 Gly Ser Tyr Gly Glu Ser Gly Val Glu Ala Phe Ile Gln Lys Ser Arg
 225 230 235 240
 Glu Asp Gly Gly Val Cys Ile Ala Gln Ser Val Lys Ile Pro Arg Glu
 245 250 255
 Pro Lys Ala Gly Glu Phe Asp Lys Ile Ile Arg Arg Leu Leu Glu Thr
 260 265 270
 Ser Asn Ala Arg Ala Val Ile Ile Phe Ala Asn Glu Asp Asp Ile Arg
 275 280 285
 Arg Val Leu Glu Ala Ala Arg Arg Ala Asn Gln Thr Gly His Phe Phe
 290 295 300
 Trp Met Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Leu His
 305 310 315 320
 Leu Glu Glu Val Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Met
 325 330 335
 Ser Val Arg Gly Phe Asp Arg Tyr Phe Ser Ser Arg Thr Leu Asp Asn
 340 345 350
 Asn Arg Arg Asn Ile Trp Phe Ala Glu Phe Trp Glu Asp Asn Phe His
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 Cys Lys Leu Ser Arg His Ala Leu Lys Lys Gly Ser His Val Lys Lys
 370 375 380
 Cys Thr Asn Arg Glu Arg Ile Gly Gln Asp Ser Ala Tyr Glu Gln Glu
 385 390 395 400
 Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ala Met Gly His Ala
 405 410 415
 Leu His Ala Met His Arg Asp Leu Cys Pro Gly Arg Val Gly Leu Cys
 420 425 430
 Pro Arg Met Asp Pro Val Asp Gly Thr Gln Leu Leu Lys Tyr Ile Arg
 435 440 445
 Asn Val Asn Phe Ser Gly Ile Ala Gly Asn Pro Val Thr Phe Asn Glu
 450 455 460
 Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Tyr Gln Tyr Gln Leu Arg

465					470								480			
Asn	Asp	Ser	Ala	Glu	Tyr	Lys	Val	Ile	Gly	Ser	Trp	Thr	Asp	His	Leu	
				485					490					495		
His	Leu	Arg	Ile	Glu	Arg	Met	His	Trp	Pro	Gly	Ser	Gly	Gln	Gln	Leu	
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Pro	Arg	Ser	Ile	Cys	Ser	Leu	Pro	Cys	Gln	Pro	Gly	Glu	Arg	Lys	Lys	
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Thr	Val	Lys	Gly	Met	Pro	Cys	Cys	Trp	His	Cys	Glu	Pro	Cys	Thr	Gly	
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Tyr	Gln	Tyr	Gln	Val	Asp	Arg	Tyr	Thr	Cys	Lys	Thr	Cys	Pro	Tyr	Asp	
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Met	Arg	Pro	Thr	Glu	Asn	Arg	Thr	Gly	Cys	Arg	Pro	Ile	Pro	Ile	Ile	
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Lys	Leu	Glu	Trp	Gly	Ser	Pro	Trp	Ala	Val	Leu	Pro	Leu	Phe	Leu	Ala	
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Val	Val	Gly	Ile	Ala	Ala	Thr	Leu	Phe	Val	Val	Ile	Thr	Phe	Val	Arg	
				595					600					605		
Tyr	Asn	Asp	Thr	Pro	Ile	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	
				610					615					620		
Val	Leu	Leu	Ala	Gly	Ile	Phe	Leu	Cys	Tyr	Ala	Thr	Thr	Phe	Leu	Met	
625					630					635					640	
Ile	Ala	Glu	Pro	Asp	Leu	Gly	Thr	Cys	Ser	Leu	Arg	Arg	Ile	Phe	Leu	
				645					650					655		
Gly	Leu	Gly	Met	Ser	Ile	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn	
				660					665					670		
Arg	Ile	Tyr	Arg	Ile	Phe	Glu	Gln	Gly	Lys	Arg	Ser	Val	Ser	Ala	Pro	
				675					680					685		
Arg	Phe	Ile	Ser	Pro	Ala	Ser	Gln	Leu	Ala	Ile	Thr	Phe	Ser	Leu	Ile	
				690					695					700		
Ser	Leu	Gln	Leu	Leu	Gly	Ile	Cys	Val	Trp	Phe	Val	Val	Asp	Pro	Ser	
705					710					715					720	
His	Ser	Val	Val	Asp	Phe	Gln	Asp	Gln	Arg	Thr	Leu	Asp	Pro	Arg	Phe	
				725					730					735		
Arg	Val	Leu	Lys	Cys	Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	Leu	Leu	
				740					745					750		
Gly	Tyr	Ser	Met	Leu	Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala	Ile	Lys	
				755					760					765		
Thr	Arg	Gly	Val	Pro	Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	Gly	Phe	
				770					775					780		
Thr	Met	Tyr	Thr	Thr	Cys	Ile	Val	Trp	Leu	Ala	Phe	Ile	Pro	Ile	Phe	
785					790					795					800	
Phe	Gly	Thr	Ser	Gln	Ser	Ala	Asp	Lys	Leu	Tyr	Ile	Gln	Thr	Thr	Thr	
				805					810					815		
Leu	Thr	Val	Ser	Val	Ser	Leu	Ser	Ala	Ser	Val	Ser	Leu	Gly	Met	Leu	
				820					825					830		
Tyr	Met	Pro	Lys	Val	Tyr	Ile	Ile	Leu	Phe	His	Pro	Glu	Gln	Asn	Thr	
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Ile	Glu	Glu	Val	Arg	Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val	Ala	
				850					855					860		
Ala	Arg	Ala	Thr	Leu	Arg	Arg	Ser	Asn	Val	Ser	Arg	Lys	Arg	Ser	Ser	
865					870					875					880	
Ser	Leu	Gly	Gly													

Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln
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 Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp
 945 950 955 960
 Glu Pro Gln Lys Asn Ala Met Ala His Gly Asn Ser Thr His Gln Asn
 965 970 975
 Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro
 980 985 990
 Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln
 995 1000 1005
 Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val
 1010 1015 1020
 Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser Ser Gln
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 Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val
 1045 1050 1055
 Asn Ser Ala Ala Ala Met Thr Leu Glu Ser Ile Met Ala Cys Cys Leu
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 Ser Glu Glu Ala Lys Glu Ala Arg Arg Ile Asn Asp Glu Ile Glu Arg
 1075 1080 1085
 Gln Leu Arg Arg Asp Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu
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 Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met
 1105 1110 1115 1120
 Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe
 1125 1130 1135
 Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile
 1140 1145 1150
 Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys
 1155 1160 1165
 Ala His Ala Gln Leu Val Arg Glu Val Asp Val Glu Lys Val Ser Ala
 1170 1175 1180
 Phe Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro
 1185 1190 1195 1200
 Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp
 1205 1210 1215
 Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala
 1220 1225 1230
 Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr
 1235 1240 1245
 Gly Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met
 1250 1255 1260
 Val Asp Val Gly Gly Gln Arg Ser Arg Lys Trp Ile His Cys Phe Glu
 1265 1270 1275 1280
 Asn Val Thr Ser Ile Met Phe Leu Val Ser Glu Tyr Asp Gln Val Leu
 1285 1290 1295
 Val Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe
 1300 1305 1310
 Arg Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu
 1315 1320 1325
 Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His
 1330 1335 1340
 Leu Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln
 1345 1350 1355 1360
 Ala Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp
 1365 1370 1375
 Ser Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu

	1380		1385		1390
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Asn	Leu	Lys	Asp	Cys	Gly
	1410		1415		

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			20					25					30			
Ser	Gln	Glu	Tyr	Ala	His	Ser	Ile	Arg	Val	Asp	Gly	Asp	Ile	Ile	Leu	
			35				40					45				
Gly	Gly	Leu	Phe	Pro	Val	His	Ala	Lys	Gly	Glu	Arg	Gly	Val	Pro	Cys	
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Gly	Glu	Leu	Lys	Lys	Glu	Lys	Gly	Ile	His	Arg	Leu	Glu	Ala	Met	Leu	
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Tyr	Ala	Ile	Asp	Gln	Ile	Asn	Lys	Asp	Pro	Asp	Leu	Leu	Ser	Asn	Ile	
				85					90					95		
Thr	Leu	Gly	Val	Arg	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala	
			100					105						110		
Leu	Glu	Gln	Ser	Leu	Thr	Phe	Val	Gln	Ala	Leu	Ile	Glu	Lys	Asp	Ala	
			115					120					125			
Ser	Asp	Val	Lys	Cys	Ala	Asn	Gly	Asp	Pro	Pro	Ile	Phe	Thr	Lys	Pro	
			130			135					140					
Asp	Lys	Ile	Ser	Gly	Val	Ile	Gly	Ala	Ala	Ala	Ser	Ser	Val	Ser	Ile	
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Met	Val	Ala	Asn	Ile	Leu	Arg	Leu	Phe	Lys	Ile	Pro	Gln	Ile	Ser	Tyr	
				165					170					175		
Ala	Ser	Thr	Ala	Pro	Glu	Leu	Ser	Asp	Asn	Thr	Arg	Tyr	Asp	Phe	Phe	
			180					185					190			
Ser	Arg	Val	Val	Pro	Pro	Asp	Ser	Tyr	Gln	Ala	Gln	Ala	Met	Val	Asp	
			195			200					205					
Ile	Val	Thr	Ala	Leu	Gly	Trp	Asn	Tyr	Val	Ser	Thr	Leu	Ala	Ser	Glu	
			210			215					220					
Gly	Asn	Tyr	Gly	Glu	Ser	Gly	Val	Glu	Ala	Phe	Thr	Gln	Ile	Ser	Arg	
225					230					235					240	
Glu	Ile	Gly	Gly	Val	Cys	Ile	Ala	Gln	Ser	Gln	Lys	Ile	Pro	Arg	Glu	
				245					250					255		
Pro	Arg	Pro	Gly	Glu	Phe	Glu	Lys	Ile	Ile	Lys	Arg	Leu	Leu	Glu	Thr	
			260					265					270			
Pro	Asn	Ala	Arg	Ala	Val	Ile	Met	Phe	Ala	Asn	Glu	Asp	Asp	Ile	Arg	
			275				280					285				
Arg	Ile	Ala	Ala	Lys	Lys	Leu	Asn	Gln	Ser	Gly	His	Phe	Leu	Trp	Ile	
			290			295					300					
Gly	Ser	Asp	Ser	Trp	Gly	Ser	Lys	Ile	Ala	Pro	Val	Tyr	Gln	Gln	Glu	
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Glu	Ile	Ala	Glu	Gly	Ala	Val	Thr	Ile	Leu	Pro	Lys	Arg	Ala	Ser	Ile	
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Asp	Gly	Phe	Asp	Arg	Tyr	Phe	Arg	Ser	Arg	Thr	Leu	Ala	Asn	Asn	Arg	
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Arg	Asn	Val	Trp	Phe	Ala	Glu	Phe	Trp	Glu	Glu	Asn	Phe	Gly	Cys	Lys
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Leu	Gly	Ser	His	Gly	Lys	Arg	Asn	Ser	His	Ile	Lys	Lys	Cys	Thr	Gly
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Leu	Glu	Arg	Ile	Ala	Arg	Asp	Ser	Ser	Tyr	Glu	Gln	Glu	Gly	Lys	Val
385						390					395				400
Gln	Phe	Val	Ile	Asp	Ala	Val	Tyr	Ser	Met	Ala	Tyr	Ala	Leu	His	Asn
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Ser	Thr	Ile	Asp	Gly	Lys	Glu	Leu	Leu	Gly	Tyr	Ile	Arg	Ala	Val	Asn
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Phe	Asn	Gly	Ser	Ala	Gly	Thr	Pro	Val	Thr	Phe	Asn	Glu	Asn	Gly	Asp
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Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Phe	Gln	Tyr	Gln	Ile	Thr	Asn	Lys	Ser
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Thr	Glu	Tyr	Lys	Val	Ile	Gly	His	Trp	Thr	Asn	Gln	Leu	His	Leu	Lys
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Val	Glu	Asp	Met	Gln	Trp	Ala	His	Arg	Glu	His	Thr	His	Pro	Ala	Ser
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Val	Cys	Ser	Leu	Pro	Cys	Lys	Pro	Gly	Glu	Arg	Lys	Lys	Thr	Val	Lys
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	530					535					540				
Gln	Val	Asp	Glu	Leu	Ser	Cys	Glu	Leu	Cys	Pro	Leu	Asp	Gln	Arg	Pro
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Asn	Met	Asn	Arg	Thr	Gly	Cys	Gln	Leu	Ile	Pro	Ile	Ile	Lys	Leu	Glu
				565					570					575	
Trp	His	Ser	Pro	Trp	Ala	Val	Val	Pro	Val	Phe	Val	Ala	Ile	Leu	Gly
			580					585					590		
Ile	Ile	Ala	Thr	Thr	Phe	Val	Ile	Val	Thr	Phe	Val	Arg	Tyr	Asn	Asp
		595					600					605			
Thr	Pro	Ile	Val	Arg	Ala	Ser	Gly	Arg	Glu	Leu	Ser	Tyr	Val	Leu	Leu
	610					615					620				
Thr	Gly	Ile	Phe	Leu	Cys	Ile	Thr	Phe	Leu	Met	Ile	Ala	Ala	Pro	Asp
625					630					635					640
Thr	Ile	Ile	Cys	Ser	Phe	Arg	Arg	Val	Phe	Leu	Gly	Leu	Gly	Met	Cys
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Phe	Ser	Tyr	Ala	Ala	Leu	Leu	Thr	Lys	Thr	Asn	Arg	Ile	His	Arg	Ile
			660					665					670		
Phe	Glu	Gln	Gly	Lys	Lys	Ser	Val	Thr	Ala	Pro	Lys	Phe	Ile	Ser	Pro
	675						680					685			
Ala	Ser	Gln	Leu	Val	Ile	Thr	Phe	Ser	Leu	Ile	Ser	Val	Gln	Leu	Leu
	690					695					700				
Gly	Val	Phe	Val	Trp	Phe	Val	Val	Asp	Pro	Pro	His	Ile	Ile	Ile	Asp
705					710					715					720
Tyr	Gly	Glu	Gln	Arg	Thr	Leu	Asp	Pro	Glu	Lys	Arg	Val	Leu	Lys	Cys
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Asp	Ile	Ser	Asp	Leu	Ser	Leu	Ile	Cys	Ser	Leu	Gly	Tyr	Ser	Ile	Leu
			740					745					750		
Leu	Met	Val	Thr	Cys	Thr	Val	Tyr	Ala	Ile	Lys	Thr	Arg	Gly	Val	Pro
		755					760					765			
Glu	Thr	Phe	Asn	Glu	Ala	Lys	Pro	Ile	Gly	Phe	Thr	Met	Tyr	Thr	Thr
	770					775					780				
Cys	Ile	Ile	Trp	Leu	Ala	Phe	Ile	Pro	Ile	Phe	Phe	Gly	Thr	Ala	Gln
785					790					795					800
Ser	Ala	Glu	Lys	Met	Tyr	Ile	Gln	Thr	Thr	Thr	Leu	Thr	Val	Ser	Met

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Ser	Leu	Ser	Ala	Ser	Val	Ser	Leu	Gly	Met	Leu	Tyr	Met	Pro	Lys	Val						
			820				825						830								
Tyr	Ile	Ile	Ile	Phe	His	Pro	Glu	Gln	Asn	Thr	Ile	Glu	Glu	Val	Arg						
			835				840						845								
Cys	Ser	Thr	Ala	Ala	His	Ala	Phe	Lys	Val	Ala	Ala	Arg	Ala	Thr	Leu						
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865				870						875			880								
Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Ile	Ser	Ser	Lys	Ser	Asn	Ser	Glu						
			885						890			895									
Asp	Pro	Phe	Pro	Gln	Pro	Glu	Arg	Gln	Lys	Gln	Gln	Gln	Pro	Leu	Ala						
			900						905			910									
Leu	Thr	Gln	Gln	Glu	Gln	Gln	Gln	Gln	Pro	Leu	Thr	Leu	Pro	Gln	Gln						
			915						920			925									
Gln	Arg	Ser	Gln	Gln	Gln	Pro	Arg	Cys	Lys	Gln	Lys	Val	Ile	Phe	Gly						
			930						935			940									
Ser	Gly	Thr	Val	Thr	Phe	Ser	Leu	Ser	Phe	Asp	Glu	Pro	Gln	Lys	Asn						
945				950						955			960								
Ala	Met	Ala	His	Gly	Asn	Ser	Thr	His	Gln	Asn	Ser	Leu	Glu	Ala	Gln						
			965						970			975									
Lys	Ser	Ser	Asp	Thr	Leu	Thr	Arg	His	Gln	Pro	Leu	Leu	Pro	Leu	Gln						
			980						985			990									
Cys	Gly	Glu	Thr	Asp	Leu	Asp	Leu	Thr	Val	Gln	Glu	Thr	Gly	Leu	Gln						
			995						1000			1005									
Gly	Pro	Val	Gly	Gly	Asp	Gln	Arg	Pro	Glu	Val	Glu	Asp	Pro	Glu	Glu						
			1010						1015			1020									
Leu	Ser	Pro	Ala	Leu	Val	Val	Ser	Ser	Ser	Gln	Ser	Phe	Val	Ile	Ser						
1025				1030						1035			1040								
Gly	Gly	Gly	Ser	Thr	Val	Thr	Glu	Asn	Val	Val	Asn	Ser	Ala	Ala	Ala						
			1045						1050			1055									
Met	Thr	Leu	Glu	Ser	Ile	Met	Ala	Cys	Cys	Leu	Ser	Glu	Glu	Ala	Lys						
			1060						1065			1070									
Glu	Ala	Arg	Arg	Ile	Asn	Asp	Glu	Ile	Glu	Arg	Gln	Leu	Arg	Arg	Asp						
			1075						1080			1085									
Lys	Arg	Asp	Ala	Arg	Arg	Glu	Leu	Lys	Leu	Leu	Leu	Leu	Gly	Thr	Gly						
			1090						1095			1100									
Glu	Ser	Gly	Lys	Ser	Thr	Phe	Ile	Lys	Gln	Met	Arg	Ile	Ile	His	Gly						
1105				1110						1115			1120								
Ser	Gly	Tyr	Ser	Asp	Glu	Asp	Lys	Arg	Gly	Phe	Thr	Lys	Leu	Val	Tyr						
			1125						1130			1135									
Gln	Asn	Ile	Phe	Thr	Ala	Met	Gln	Ala	Met	Ile	Arg	Ala	Met	Asp	Thr						
			1140						1145			1150									
Leu	Lys	Ile	Pro	Tyr	Lys	Tyr	Glu	His	Asn	Lys	Ala	His	Ala	Gln	Leu						
			1155						1160			1165									
Val	Arg	Glu	Val	Asp	Val	Glu	Lys	Val	Ser	Ala	Phe	Glu	Asn	Pro	Tyr						
			1170						1175			1180									
Val	Asp	Ala	Ile	Lys	Ser	Leu	Trp	Asn	Asp	Pro	Gly	Ile	Gln	Glu	Cys						
1185				1190						1195			1200								
Tyr	Asp	Arg	Arg	Arg	Glu	Tyr	Gln														

Gln Arg Ser Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr Ser Ile
 1265 1270 1275 1280
 Met Phe Leu Val Ser Glu Tyr Asp Gln Val Leu Val Glu Ser Asp Asn
 1285 1290 1295
 Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr
 1300 1305 1310
 Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys
 1315 1320 1325
 Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Val Asp Tyr Phe
 1330 1335 1340
 Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala Ala Arg Glu Phe
 1345 1350 1355 1360
 Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser Asp Lys Ile Ile
 1365 1370 1375
 Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val
 1380 1385 1390
 Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Lys Asp Cys
 1395 1400 1405
 Gly Leu Phe
 1410

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000